GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 21, 2004, 09:14:54 ; Search time 1.05545 Seconds
(without alignments)
601.551 Million cell updates/sec

Title: US-09-869-414A-66
Perfect score: 20
Sequence: 1 NLDA 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	4	22	AAE06901	Human amyloid prec
2	20	100.0	4	22	AAU06630	Asp2 recognition s
3	20	100.0	4	22	AAU07229	Human beta-amyloid
4	20	100.0	4	23	ABB06547	Beta-secretase rel
5	20	100.0	5	17	AAW00415	Interleukin-6 anta
6	20	100.0	5	18	AAW08217	Swedish double mut
7	20	100.0	5	19	AAW61151	APP Swedish double
8	20	100.0	5	20	AAY33751	Swedish mutant bet
9	20	100.0	5	22	AAB47261	Swedish mutation A
10	20	100.0	6	23	AAU78500	Beta secretase cle
11	20	100.0	8	21	AAY94771	Beta-secretase sub
12	20	100.0	8	22	AAE10661	Human aspartyl pro
13	20	100.0	8	22	AAE02613	Human Aspartyl pro
14	20	100.0	8	23	ABB78622	Human beta secreta
15	20	100.0	9	19	AAW82081	Fluorogenic protea
16	20	100.0	9	21	AAB07874	A peptide fragment
17	20	100.0	9	21	AAB07894	Substrate for beta
18	20	100.0	9	22	AAG73297	Protease indicator
19	20	100.0	9	23	ABU60429	Protease binding p
20	20	100.0	9	23	ABU60441	Protease binding p
21	20	100.0	9	23	ABB09003	Peptide #1 used as
22	20	100.0	9	23	ABB06519	Beta-secretase rel
23	20	100.0	9	23	AAM50897	Oligopeptide subst
24	20	100.0	9	23	ABB07598	Synthetic oligopep
25	20	100.0	9	23	AAE16663	Oligopeptide subst
26	20	100.0	9	23	AAU74837	Synthetic amyloid
27	20	100.0	9	24	ABP71630	Beta-secretase act
28	20	100.0	9	24	ABG75940	Synthetic Amyloid
29	20	100.0	9	24	ABP71468	Beta-secretase cle
30	20	100.0	9	24	ABP71952	Antigenic peptide
31	20	100.0	9	24	ABP71953	Antigenic peptide
32	20	100.0	9	24	ABP57515	Differentially iso
33	20	100.0	9	24	ABP71269	Oligopeptide subst
34	20	100.0	9	24	AAO16449	Beta-secretase syn
35	20	100.0	9	24	AAO26801	Beta-secretase sub
36	20	100.0	9	24	ABP57084	Synthetic oligopep
37	20	100.0	9	24	ABP58375	Beta-secretase amy
38	20	100.0	10	18	AAW08362	Beta-secretase sub
39	20	100.0	10	20	AAY33756	Synthetic oligopep
40	20	100.0	10	21	AAY69707	Beta-APP alpha-sec
41	20	100.0	10	22	AAE10653	Human APP-Sw beta-
42	20	100.0	10	22	AAE06898	Human amyloid prec
43	20	100.0	10	22	AAU06627	Synthetic Asp2 rec
44	20	100.0	10	22	AAU07226	Human beta-amyloid
45	20	100.0	10	22	AAE02605	Human APP-Sw beta-

ALIGNMENTS

RESULT 1
AAE06901
ID AAE06901 standard; peptide; 4 AA.
XX
AC AAE06901;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human amyloid precursor protein (APP-Sw) beta-secretase peptide #2.
XX
KW Human; aspartyl protease 2; Asp 2; beta-amyloid precursor protein;
KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW neuroprotective; antisense therapy; APP-Sw; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200150829-A2.
XX
PD 19-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB00799.
XX
PR 09-MAY-2001; 2001WO-IB00799.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-483072/52.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity -
XX
PS Claim 129; Page 101; 185pp; English.
XX
CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing
CC therapeutics for the treatment and prevention of Alzheimer's disease,
CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying
CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting
CC Hu-Asp nucleic acids in in vitro assays and in Northern and Southern

CC blots. The present sequence is human amyloid precursor protein (APP-Sw)
CC beta-secretase peptide related to the invention.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLDA 4
||||
Db 1 NLDA 4

RESULT 2
AAU06630
ID AAU06630 standard; Peptide; 4 AA.
XX
AC AAU06630;
XX
DT 24-OCT-2001 (first entry)
XX
DE Asp2 recognition site from APP-SW.
XX
KW Aspartyl protease; Asp2; beta-secretase; nootropic;
KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW amyloid-beta; Abeta; APP-SW.
XX
OS Homo sapiens.
XX
PN WO200149098-A2.
XX
PD 12-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB00798.
XX
PR 09-MAY-2001; 2001WO-IB00798.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-502549/55.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity -
XX
PS Claim 129; Page 101; 185pp; English.
XX
CC The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2

CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp
CC proteins and vectors expressing them, and a polypeptide (isoform of
CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
CC APP or its fragment containing an APP cleavage site recognizable by a
CC mammalian beta-secretase, and further comprising two lysine residues at
CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
CC APP fragment. Also included in the invention are methods of identifying
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC useful for treating Alzheimer's disease. APP is useful in methods for
CC identifying inhibitors or modulators of human Asp2 activity and
CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
CC therapeutics for the treatment or prevention of Alzheimer's disease.
CC APP comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which
CC is associated with increased levels of Abeta processing is useful in
CC assays relating the Alzheimer's research. The expression vector is useful
CC for recombinantly expressing APP. Nucleic acids that hybridise to
CC Asp oligonucleotides are useful as probes or primers. The probes are
CC useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC Northern and Southern blots. The present sequence is the APP
CC beta-secretase peptide sequence from APP-SW, the Swedish mutation.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLDA 4
||||
Db 1 NLDA 4

RESULT 3
AAU07229
ID AAU07229 standard; Peptide; 4 AA.
XX
AC AAU07229;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human beta-amyloid protein precursor, APP-beta secretase site peptide #2.
XX
KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW beta-secretase; Alzheimer's disease; APP-beta.
XX
OS Homo sapiens.
XX
PN WO200149097-A2.
XX
PD 12-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB00797.
XX
PR 09-MAY-2001; 2001WO-IB00797.

XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-502548/55.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity -
XX
PS Claim 129; Page 101; 185pp; English.
XX
CC The invention relates to a novel purified polypeptide comprising a
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC and the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. Also included is an isoform of amyloid protein precursor (APP)
CC comprising the amino acid sequence of a APP or its fragment containing
CC an APP cleavage site recognisable by a mammalian beta-secretase, and
CC further comprising two lysine residues at the carboxyl terminus of the
CC amino acid sequence of the mammalian APP or APP fragment. The
CC polypeptides are used for assaying for modulators of beta-secretase
CC activity; identifying agents that inhibit the APP processing activity
CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
CC modulate the activity of Asp2; and for reducing cellular production of
CC amyloid beta (Abeta) from APP. Agents identified by the above methods
CC are useful for treating Alzheimer's disease; and for identifying
CC modulators of amyloid-beta (Abeta) peptide production, for use in
CC designing therapeutics for the treatment or prevention of Alzheimer's
CC disease. Probes and primers derived from Asp nucleic acid sequences
CC are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC Northern and Southern blots. The present sequence represents the
CC amino acid sequence of human amyloid protein precursor, APP-beta
CC secretase site peptide substrate #2 used in assays of human Asp2 beta-
CC secretase activity.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 NLDA 4
              ||||
Db          1 NLDA 4
```

RESULT 4
ABB06547
ID ABB06547 standard; Peptide; 4 AA.
XX

AC ABB06547;
XX
DT 31-MAY-2002 (first entry)
XX
DE Beta-secretase related peptide SEQ ID NO:142.
XX
KW Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;
KW aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;
KW Alzheimer's disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200206306-A2.
XX
PD 24-JAN-2002.
XX
PF 19-JUL-2001; 2001WO-US23035.
XX
PR 19-JUL-2000; 2000US-219795P.
PR 12-MAR-2001; 2001US-275251P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
PI Heinrikson RL;
XX
DR WPI; 2002-216995/27.
XX
PT Novel substrates for human aspartyl protease useful for identifying
PT modulators of beta secretase activity of aspartyl protease for treating
PT Alzheimer's disease -
XX
PS Disclosure; Page 169; 188pp; English.
XX
CC The present invention describes an isolated peptide (I) comprising a
CC sequence of at least four amino acids, where the peptide is a substrate
CC for conducting aspartyl protease assays. (I) has neuroprotective and
CC nootropic activities, and can be used as an inhibitor of beta-secretase
CC activity. A beta-secretase modulator from the present invention can be
CC used for inhibiting beta-secretase activity in vivo, and in the
CC manufacture of a medicament for the treatment of Alzheimer's disease.
CC Pharmaceutical compositions from the present invention can be used for
CC treating a disease or condition characterised by an abnormal beta-
CC secretase activity. (I) is useful for identifying agents that modulate
CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful
CC as a core structure to construct derivatives. ABL49914 to ABL49925 and
CC ABB06409 to ABB06593 represent sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 23; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLDA 4

```
              ||||
Db          1 NLDA 4


RESULT 5
AAW00415
ID   AAW00415 standard; peptide; 5 AA.
XX
AC   AAW00415;
XX
DT   29-AUG-1996  (first entry)
XX
DE   Interleukin-6 antagonist peptide.
XX
KW   IL-6; antagonist; autoimmune disease.
XX
OS   Synthetic.
XX
PN   JP07324097-A.
XX
PD   12-DEC-1995.
XX
PF   30-MAY-1994;   94JP-0117259.
XX
PR   30-MAY-1994;   94JP-0117259.
XX
PA   (DAIL ) DAICEL CHEM IND LTD.
PA   (FUJI ) FUJISAWA PHARM CO LTD.
XX
DR   WPI; 1996-065476/07.
XX
PT   Interleukin 6 antagonist - useful for treating auto:immune diseases
XX
PS   Claims 3, 6; Pages 2, 3; 19pp; Japanese.
XX
CC   New IL-6 antagonists are provided which are of formula X-W-Y, in
CC   which X is H or an amino-protecting group, Y is OH or a carboxy-
CC   protecting group, and W is a peptide containing all or part of the
CC   sequence as given in AAW00401, AAW00402, AAW00403 or AAW00404, where any
CC   free mercapto groups in the sequence are optionally protected. The
CC   present sequence is a specifically preferred partial sequence of AAW00402
CC   and is itself claimed as a new chemical entity.
CC   The IL-6 antagonists are useful for treating autoimmune diseases.
XX
SQ   Sequence   5 AA;

  Query Match             100.0%;  Score 20;  DB 17;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          2 NLDA 5


RESULT 6
AAW08217
```

ID AAW08217 standard; peptide; 5 AA.
XX
AC AAW08217;
XX
DT 05-SEP-1997 (first entry)
XX
DE Swedish double mutant APP beta-cleavage site.
XX
KW Beta-cleavage site; beta amyloid precursor protein; APP; beta-secretase;
KW alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO9640885-A2.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US09985.
XX
PR 07-JUN-1995; 95US-0485152.
PR 07-JUN-1995; 95US-0480498.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Anderson JP, Chrysler SMS, Jacobson-croak KL, Keim PS;
PI Mcconlogue LC, Sinha S, Tan H;
XX
DR WPI; 1997-052304/05.
XX
PT Beta-secretase which specifically cleaves beta-amyloid precursor
PT protein - useful to screen for inhibitors useful in treatment of
PT Alzheimer's disease
XX
PS Claim 5; Page 60; 92pp; English.
XX
CC AAW08216, AAW08217 and AAW08350 represent beta-cleavage sites from
CC beta-amyloid precursor proteins (APP). These sequences are recognised by
CC the enzyme of the invention. The enzyme of the invention is
CC beta-secretase, and specifically cleaves beta-APP at one of these sites.
CC Normal processing of beta-APP is thought to occur via cleavage between
CC residues 16 and 17 of the beta-amyloid peptide region by an
CC alpha-secretase. Pathogenic processing is thought to occur by
CC beta-secretase cleavage of beta-APP. Beta-secretase activity can be
CC detected and measured using a method of the invention, which detects at
CC least one of the beta-secretase cleavage products formed on cleavage. The
CC method can be used to determine whether a test substance inhibits
CC proteolytic cleavage, by beta-secretase, of beta-APP. Compounds effective
CC to at least partially inhibit beta-secretase activity can be used to
CC inhibit cleavage of beta-APP in cells or mammalian hosts. Isolation and
CC purification of beta-secretase will permit chemical modelling of a
CC critical event in the pathology of Alzheimer's disease.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 20; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 NLDA 4
              ||||
Db          2 NLDA 5


RESULT 7
AAW61151
ID   AAW61151 standard; Peptide; 5 AA.
XX
AC   AAW61151;
XX
DT   26-OCT-1998  (first entry)
XX
DE   APP Swedish double mutation cleavage site.
XX
KW   Beta-secretase; human; beta-amyloid precursor protein; APP;
KW   protease; inhibitor; screening; Alzheimer's disease; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9826059-A1.
XX
PD   18-JUN-1998.
XX
PF   11-DEC-1996;   96WO-US19549.
XX
PR   11-DEC-1996;   96WO-US19549.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Anderson JP,  Chrysler SMS,  Keim PS,  Sinha S;
XX
DR   WPI; 1998-348519/30.
XX
PT   Novel beta-secretase which cleaves beta-amyloid precursor protein -
PT   useful for screening for compounds which inhibit the cleavage and
PT   are useful for treating Alzheimer's disease
XX
PS   Disclosure; Page 20; 39pp; English.
XX
CC   This peptide comprises the site of the 'Swedish' double mutation
CC   beta-amyloid precursor protein (APP) (MBP-C125 SW) that is cleaved
CC   by a novel beta-secretase isolated from human 293 cells.  This
CC   protease cleaves APP at the N-terminus of the beta-amyloid peptide
CC   (beta-AP) and is believed to be the putative beta-secretase
CC   responsible for the pathogenic processing of APP to beta-AP in
CC   Alzheimer's disease, Down's syndrome and HCHWA-D.  Recombinant
CC   fusion proteins (see AAW61152) were generated comprising the last
CC   125 amino acids of APP (wild-type (see AAW61150) or Swedish double
CC   mutation) fused to the C-terminal end of maltose binding protein.
CC   The fusion proteins were expressed in Escherichia coli, and used as
CC   substrates for beta-secretase in beta-secretase inhibitor assays.
CC   Compounds that inhibit APP cleavage by beta-secretase may be useful
CC   in the treatment of Alzheimer's disease.
XX
SQ   Sequence   5 AA;
```

```
  Query Match             100.0%;  Score 20;  DB 19;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          2 NLDA 5


RESULT 8
AAY33751
ID   AAY33751 standard; Protein; 5 AA.
XX
AC   AAY33751;
XX
DT   09-NOV-1999  (first entry)
XX
DE   Swedish mutant beta-amyloid protein precursor (APP) cleavage site.
XX
KW   Beta-secretase; beta-amyloid protein precursor; APP; Down's syndrome;
KW   Alzheimer's disease; cleavage site; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US5942400-A.
XX
PD   24-AUG-1999.
XX
PF   07-JUN-1996;   96US-0659984.
XX
PR   07-JUN-1996;   96US-0659984.
PR   07-JUN-1995;   95US-0480498.
PR   07-JUN-1995;   95US-0485152.
XX
PA   (ELAN-) ELAN PHARM INC.
XX
PI   Anderson JP,  Jacobson-Croak KL,  Sinha S;
XX
DR   WPI; 1999-517417/43.
XX
PT   A method for detecting human beta-secretase cleavage of polypeptides
PT   useful for identifying beta-secretase inhibitors
XX
PS   Examples; Column 28; 43pp; English.
XX
CC   This sequence is the Swedish mutant beta-amyloid protein precursor (APP)
CC   cleavage site. APP is cleaved by beta-secretase AAY33741. The wild type
CC   cleavage site AAY33750 and the Swedish mutant version are used in a
CC   method for detecting human beta-secretase cleavage of polypeptides and
CC   for identifying beta-secretase inhibitors. Inhibition of beta-secretase
CC   activity would be useful for chemical modelling of a critical event in
CC   the pathology of Alzheimer's disease. Inhibitors of beta-secretase would
CC   be useful for the prevention and treatment of Alzheimer's disease and
CC   Down's Syndrome.
XX
```

SQ Sequence 5 AA;

Query Match 100.0%; Score 20; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 NLDA 4
              ||||
Db          2 NLDA 5
```

RESULT 9
AAB47261
ID AAB47261 standard; Peptide; 5 AA.
XX
AC AAB47261;
XX
DT 18-JUL-2001 (first entry)
XX
DE Swedish mutation APP sequence for cleavage by beta-secretase.
XX
KW Beta-secretase; isotype; beta-amyloid precursor protein; APP;
KW beta-amyloid peptide; beta-AP; Alzheimer's disease; Downs syndrome;
KW HCHWA-D; Swedish mutation; maltose binding protein; MBP.
XX
OS Homo sapiens.
XX
PN US6221645-B1.
XX
PD 24-APR-2001.
XX
PF 07-JUN-1996; 96US-0660531.
XX
PR 07-JUN-1995; 95US-0480498.
XX
PA (ELAN-) ELAN PHARM INC.
XX
PI Chrysler SMS, Sinha S, Keim PS, Anderson JP, Tan H, McConlogue LC;
XX
DR WPI; 2001-315578/33.
XX
PT Novel antibody that specifically binds native beta-secretase protein,
PT useful for raising anti-idiotypic antibodies and for detecting or
PT diagnosing pathological conditions related to presence of respective
PT antigens -
XX
PS Example; Column 28; 42pp; English.
XX
CC The sequences given in AAB47260-61 represent cleavage sites derived
CC from wild-type and the Swedish mutation of beta-amyloid precursor
CC protein (APP). These cleavage sites were used in fusion proteins
CC which were used as substrates for the beta-secretase protein which
CC is characterized by an ability to cleave the 695-amino acid isotype
CC of APP between amino acids 596 and 597. The fusion proteins contain
CC the carboxy-terminal end of Maltose binding protein (MBP) fused to
CC the carboxy-terminal 125 amino acids of either wild type APP or APP
CC containing the Swedish mutation. Beta-secretase is thought to be

CC responsible for the pathogenic processing of APP to form beta amyloid
CC peptide (beta-AP) in beta-AP related conditions, e.g. Alzheimer's
CC disease, Downs syndrome, HCHWA-D etc. Beta-secretase has a molecular
CC weight of 260-300 kD and will bind to wheat germ agglutinin but not to
CC concanavalin A. Beta-secretase will cleave both the wild type and
CC the Swedish mutation of APP.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 20; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 NLDA 4
              ||||
Db          2 NLDA 5
```

RESULT 10
AAU78500
ID AAU78500 standard; Peptide; 6 AA.
XX
AC AAU78500;
XX
DT 18-JUN-2002 (first entry)
XX
DE Beta secretase cleavage site of beta APP Swedish mutant.
XX
KW Alzheimer's disease; APP; beta amyloid precursor protein; beta secretase;
KW BACE; beta-site APP cleaving enzyme; human; nootropic; neuroprotective;
KW beta-site amyloid precursor protein (APP)-cleaving enzyme;
KW BACE secretase/sheddase; neurodegenerative disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Cleavage-site 4..5
FT /note= "Beta secretase cleavage site"
XX
PN WO200210354-A2.
XX
PD 07-FEB-2002.
XX
PF 01-AUG-2001; 2001WO-CA01118.
XX
PR 01-AUG-2000; 2000CA-2313828.
XX
PA (RECL-) INST RECH CLINIQUES MONTREAL.
XX
PI Seidah NG, Chretien M, Cromlish JA;
XX
DR WPI; 2002-280632/32.
XX
PT Modulating activity of beta-site amyloid precursor protein-cleaving
PT enzyme secretase/sheddase for treatment of neurodegenerative disorder
PT characterised by generation of Abeta protein, by preventing cleavage of
PT enzyme -

XX
PS Disclosure; Page 2; 64pp; English.
XX
CC This invention relates to a novel method for modulating activity of
CC beta-site amyloid precursor protein (APP)-cleaving enzyme (BACE)
CC secretase/sheddase. Cleavage of BACE by this enzyme results in the
CC generation of a soluble BACE which enhances the production of the
CC amyloidogenic peptide Abeta which has been shown to be involved in the
CC aetiology of Alzheimer's disease. Inhibition of BACE secretase can be
CC achieved by administration of an antisense nucleotide molecule capable
CC of hybridising with BACE mRNA, by using a ribozyme that targets and
CC degrades BACE secretase mRNA, with a peptide that can interfere with
CC binding of the enzyme with BACE or using an antibody or antagonist that
CC can function as an inhibitor of BACE secretase activation. The methods
CC of the invention modulate the activity of BACE secretase/sheddase by
CC preventing cleavage of BACE, which is useful for the treatment of a
CC neurodegenerative disorder characterised by the generation of Abeta
CC protein, especially Alzheimer's disease. The invention also comprises a
CC method for identification of an agent that can alter the ability of BACE
CC secretase to associate with and process a known substrate, this method
CC can be used for high throughput screening of candidate molecules. The
CC invention also comprises a method for determining whether an individual
CC is at risk of developing a neurodegenerative disorder characterised
CC by the generation of Abeta protein by measuring the levels of BACE
CC C terminal cleavage products in a sample or tissue where an increase
CC in cleavage products indicates a person at risk. The present sequence
CC represents the beta secretase cleavage site of the Swedish mutant of
CC beta amyloid precursor protein.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 20; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 NLDA 4
              ||||
Db          3 NLDA 6
```

RESULT 11
AAY94771
ID AAY94771 standard; Protein; 8 AA.
XX
AC AAY94771;
XX
DT 12-FEB-2001 (first entry)
XX
DE Beta-secretase substrate peptide SEQ ID 17.
XX
KW Beta-secretase; enzyme; amyloid plaque; Alzheimer's disease;
KW Down's syndrome; amyloid angiopathy; gene therapy; neuroprotective.
XX
OS Synthetic.
XX
PN WO200058479-A1.
XX

PD 05-OCT-2000.
XX
PF 23-MAR-2000; 2000WO-US07755.
XX
PR 26-MAR-1999; 99US-0277229.
XX
PA (AMGE-) AMGEN INC.
XX
PI Citron M, Vassar RJ, Bennett BD;
XX
DR WPI; 2000-594643/56.
XX
PT Isolated beta-secretase nucleic acids and encoded polypeptides, useful
PT for diagnosis and gene therapy of Alzheimer's disease -
XX
PS Example 10; Page 117; 145pp; English.
XX
CC This invention relates to 3 nucleotide sequences encoding beta-secretase
CC proteins. Beta-secretase is an enzyme involved in the production of one
CC of the components of amyloid plaques involved in Alzheimer's disease. The
CC invention includes an expression vector comprising the nucleotide
CC sequence, a host cell comprising the expression vector, and a process for
CC producing the protein through culturing the transformed cells. Also
CC included in the invention are a polypeptide derivative of the
CC beta-secretase protein, a fusion protein comprising beta-secretase fused
CC to a heterologous amino acid sequence, and a method for modulating the
CC levels of beta-secretase polypeptide in a mammal comprising administering
CC the polynucleotide sequence. Beta-secretase exhibits neuroprotective and
CC nootropic activity. The beta-secretase nucleotide sequence may be used to
CC map locations of the beta-secretase gene and related genes on chromosomes
CC and as hybridization probes in diagnostic assays to test for the presence
CC of beta-secretase DNA or RNA, such as in Alzheimer's disease, Down's
CC syndrome, and amyloid angiopathy. The nucleotide sequence may also be
CC used as anti-sense inhibitors of beta-secretase expression, in gene
CC therapy of Alzheimer's disease, and for the identification of compounds
CC that modulate beta-secretase activity. Antibodies to the beta-secretase
CC protein may be used for in vitro and in vivo diagnostic purposes to
CC detect the presence of beta-secretase polypeptide in a body fluid or cell
CC sample. The present sequence represents a beta-secretase substrate
CC peptide.
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 20; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLDA 4
||||
Db 3 NLDA 6

RESULT 12
AAE10661
ID AAE10661 standard; peptide; 8 AA.
XX
AC AAE10661;

XX

DT 10-DEC-2001 (first entry)

XX

DE Human aspartyl protease-1 beta-secretase Swedish mutant peptide.

XX

KW Human; aspartyl protease 1; Aspl; amyloid precursor protein; APP;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW aspartyl protease-1 beta-secretase Swedish mutant peptide.

XX

OS Homo sapiens.
OS Synthetic.

XX

FH Key Location/Qualifiers
FT Cleavage-site 4..5

XX

PN GB2357767-A.

XX

PD 04-JUL-2001.

XX

PF 22-SEP-2000; 2000GB-0023315.

XX

PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Bienkowkski MJ, Gurney M;

XX

DR WPI; 2001-444208/48.

XX

PT Polypeptide comprising fragments of human aspartyl protease with
PT amyloid precursor protein processing activity and alpha-secretase
PT activity, for identifying modulators useful in treating Alzheimer's
PT disease -

XX

PS Example 15; Page 92; 187pp; English.

XX

CC The patent discloses human aspartyl protease 1 (hu-Aspl) or modified
CC Aspl proteins which lack transmembrane domain or amino terminal
CC domain or cytoplasmic domain and retains alpha-secretase activity
CC and amyloid protein precursor (APP) processing activity. The proteins
CC of the invention are useful for assaying hu-Aspl alpha-secretase
CC activity, which in turn is useful for identifying modulators of
CC hu-Aspl alpha-secretase activity, where modulators that increase
CC hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Aspl protease substrate is useful for assaying
CC hu-Aspl proteolytic activity, by contacting hu-Aspl protein with
CC the substrate under acidic conditions and determining the level of
CC hu-Aspl proteolytic activity. The present sequence is human aspartyl
CC protease-1 (hu-Asp-1) beta-secretase Swedish (Sw) mutant peptide
CC which is used for determining the enzymatic activity of Asp-1 protein

CC lacking a transmembrane (TM) domain and containing (His)6 tag.
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 20; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLDA 4
||||
Db 3 NLDA 6

RESULT 13
AAE02613
ID AAE02613 standard; peptide; 8 AA.
XX
AC AAE02613;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human Aspartyl protease-1 beta-secretase Swedish mutant form peptide.
XX
KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Asp1;
KW beta-secretase.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Cleavage-site 4..5
XX
PN WO200123533-A2.
XX
PD 05-APR-2001.
XX
PF 22-SEP-2000; 2000WO-US26080.
XX
PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney M, Bienkowski MJ;
XX
DR WPI; 2001-290516/30.
XX
PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT protein, useful for the treatment of Alzheimer's disease -
XX
PS Example 15; Page 94; 189pp; English.
XX
CC The present invention relates to enzymes for cleaving the alpha-
CC secretase site of the amyloid precursor protein (APP) and methods of
CC identifying those enzymes. The methods may be used to identify enzymes

CC that may be used to cleave the alpha-secretase cleavage site of the APP
CC protein. The enzymes may be used to treat or modulate the progress of
CC Alzheimer's disease. The present sequence is human Aspartyl protease-1
CC (hu-Asp-1) beta-secretase, Swedish (Sw) mutant form peptide which is used
CC for determining the enzymatic activity of Asp-1 deltaTM (His)6 protein.
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 20; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 NLDA 4
              ||||
Db          3 NLDA 6
```

RESULT 14
ABB78622
ID ABB78622 standard; Peptide; 8 AA.
XX
AC ABB78622;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human beta secretase peptide SEQ ID NO:71.
XX
KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
KW proteolytic.
XX
OS Homo sapiens.
XX
PN GB2367060-A.
XX
PD 27-MAR-2002.
XX
PF 29-OCT-2001; 2001GB-0025934.
XX
PR 23-SEP-1999; 99US-155493P.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-169232P.
PR 22-SEP-2000; 2000GB-0023315.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowkski MJ, Gurney M;
XX
DR WPI; 2002-396337/43.
XX
PT Human aspartyl protease 1 substrates useful in assays to detect
PT aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
PT disease -
XX
PS Example 15; Page 92; 182pp; English.
XX

CC The present invention describes a human aspartyl protease 1 (hu-Asp1) substrate (I) which comprises a peptide of no more than 50 amino acids, and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1 proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with (I) under acidic conditions; and (b) determining the level of hu-Asp1 proteolytic activity; (2) a purified polynucleotide (III) comprising a nucleotide sequence that hybridises under stringent conditions to the non-coding strand complementary to a defined 1804 nucleotide sequence (see ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane domain); (3) a purified polynucleotide (III') comprising a sequence that hybridises under stringent conditions to (III) (the nucleotide sequence encodes a polypeptide further lacking a pro-peptide domain corresponding to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV) comprising (III) or (III'); and (5) a host cell (V) transformed or transfected with (III), (III') and/or (IV). The hu-Asp1 protease substrate (I) may be used as an enzyme substrate in assays to detect aspartyl protease activity, (II) and therefore diagnose diseases associated with aberrant hu-Asp1 expression and activity such as Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present sequence represents a human beta secretase peptide, which is used in an example from the present invention.
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 20; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 NLDA 4
              ||||
Db          3 NLDA 6
```

RESULT 15
AAW82081
ID AAW82081 standard; peptide; 9 AA.
XX
AC AAW82081;
XX
DT 18-FEB-1999 (first entry)
XX
DE Fluorogenic protease indicator protease binding peptide #59.
XX
KW Protease activity; fluorphore; detection; fluorogenic; cellular uptake;
KW conformation change.
XX
OS Synthetic.
XX
PN WO9837226-A1.
XX
PD 27-AUG-1998.
XX
PF 20-FEB-1998; 98WO-US03000.
XX

PR 20-FEB-1997; 97US-0802981.
XX
PA (ONCO-) ONCOIMMUNIN INC.
XX
PI Komoriya A, Packard BS;
XX
DR WPI; 1998-467579/40.
XX
PT New fluorogenic compositions - containing 2 fluorophores separated
PT by a peptide comprising a protease binding site, used for detecting
PT protease activity in samples.
XX
PS Claim 4; Page 77; 90pp; English.
XX
CC AAW82023-W82240 are peptides used in the construction of a fluorogenic
CC composition which is used for the detection of protease activity in
CC biological samples. The products can be used for the detection of
CC conformation changes in nucleic acids, oligosaccharides,
CC polysaccharides, proteins, peptides, lipids, phopholipids, glycolipids,
CC glycoproteins, steroids or polymers. In addition, attachment of a
CC hydrophobic group to a molecule can be used to enhance uptake by cells.
CC The composition is composed of P = peptide comprising a protease binding
CC site for the protease, F1, F2 peptides = fluorophores where F1 is
CC attached to the amino terminal amino acid and F2 is attached to the
CC carboxyl terminal amino acid and S1, S2 peptides = when present, are
CC peptide spacers where S1, when present, is attached to the amino terminal
CC acid, and S2, when present, is attached to the carboxyl terminal amino
CC acid.
XX
SQ Sequence 9 AA;

  Query Match 100.0%; Score 20; DB 19; Length 9;
  Best Local Similarity 100.0%; Pred. No. 9.3e+05;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLDA 4
      ||||
Db 4 NLDA 7

Search completed: January 21, 2004, 09:22:26
Job time : 2.05545 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 21, 2004, 09:19:55 ; Search time 0.359465 Seconds
(without alignments)
470.821 Million cell updates/sec

Title: US-09-869-414A-66
Perfect score: 20
Sequence: 1 NLDA 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	4	4	US-09-548-372D-66	Sequence 66, Appl
2	20	100.0	4	4	US-09-548-367D-66	Sequence 66, Appl
3	20	100.0	4	4	US-09-551-853D-66	Sequence 66, Appl
4	20	100.0	5	1	US-08-480-498-2	Sequence 2, Appli
5	20	100.0	5	2	US-08-659-984A-14	Sequence 14, Appl
6	20	100.0	5	3	US-08-660-531-14	Sequence 14, Appl
7	20	100.0	5	4	US-09-054-334-2	Sequence 2, Appli
8	20	100.0	9	3	US-08-802-981-219	Sequence 219, App
9	20	100.0	10	2	US-08-659-984A-19	Sequence 19, Appl
10	20	100.0	10	3	US-08-660-531-19	Sequence 19, Appl
11	20	100.0	10	4	US-09-548-372D-63	Sequence 63, Appl

12	20	100.0	10	4	US-09-548-367D-63	Sequence 63, Appl
13	20	100.0	10	4	US-09-551-853D-63	Sequence 63, Appl
14	20	100.0	10	4	US-09-604-608-5	Sequence 5, Appli
15	20	100.0	11	5	PCT-US94-07043A-3	Sequence 3, Appli
16	20	100.0	19	4	US-09-376-330-12	Sequence 12, Appl
17	20	100.0	21	2	US-08-659-984A-18	Sequence 18, Appl
18	20	100.0	21	3	US-08-802-981-112	Sequence 112, App
19	20	100.0	21	3	US-08-660-531-18	Sequence 18, Appl
20	20	100.0	30	2	US-08-659-984A-17	Sequence 17, Appl
21	20	100.0	30	3	US-08-433-522A-17	Sequence 17, Appl
22	20	100.0	30	3	US-09-135-166-17	Sequence 17, Appl
23	20	100.0	30	3	US-08-660-531-17	Sequence 17, Appl
24	20	100.0	30	3	US-08-942-046-17	Sequence 17, Appl
25	20	100.0	33	1	US-08-438-753B-18	Sequence 18, Appl
26	20	100.0	33	1	US-08-443-883A-18	Sequence 18, Appl
27	20	100.0	33	2	US-08-631-328-18	Sequence 18, Appl
28	20	100.0	33	2	US-08-455-524B-18	Sequence 18, Appl
29	20	100.0	33	2	US-08-659-984A-16	Sequence 16, Appl
30	20	100.0	33	2	US-08-455-021B-18	Sequence 18, Appl
31	20	100.0	33	3	US-09-045-467-18	Sequence 18, Appl
32	20	100.0	33	3	US-08-660-531-16	Sequence 16, Appl
33	20	100.0	42	2	US-08-659-984A-15	Sequence 15, Appl
34	20	100.0	42	3	US-08-660-531-15	Sequence 15, Appl
35	20	100.0	44	3	US-08-905-223-345	Sequence 345, App
36	20	100.0	46	3	US-08-924-330A-10	Sequence 10, Appl
37	20	100.0	46	3	US-09-138-721-10	Sequence 10, Appl
38	20	100.0	50	4	US-09-205-258-493	Sequence 493, App
39	20	100.0	57	1	US-08-370-225-29	Sequence 29, Appl
40	20	100.0	57	1	US-08-370-225-30	Sequence 30, Appl
41	20	100.0	57	1	US-08-461-859-29	Sequence 29, Appl
42	20	100.0	57	1	US-08-461-859-30	Sequence 30, Appl
43	20	100.0	57	5	PCT-US93-10069-29	Sequence 29, Appl
44	20	100.0	57	5	PCT-US93-10069-30	Sequence 30, Appl
45	20	100.0	62	3	US-08-995-156A-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-09-548-372D-66
; Sequence 66, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23

```
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
US-09-548-372D-66

  Query Match             100.0%;  Score 20;  DB 4;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          1 NLDA 4


RESULT 2
US-09-548-367D-66
; Sequence 66, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
US-09-548-367D-66

  Query Match             100.0%;  Score 20;  DB 4;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
```

```
Db          1 NLDA 4


RESULT 3
US-09-551-853D-66
; Sequence 66, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280L
;  CURRENT APPLICATION NUMBER: US/09/551,853D
;  CURRENT FILING DATE:  2000-04-18
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
US-09-551-853D-66

  Query Match             100.0%;  Score 20;  DB 4;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          1 NLDA 4


RESULT 4
US-08-480-498-2
; Sequence 2, Application US/08480498
; Patent No. 5744346
;  GENERAL INFORMATION:
;    APPLICANT:  Chrysler, Susanna M.S.
;    APPLICANT:  Sinha, Sukanto
;    APPLICANT:  Keim, Pamela S.
;    APPLICANT:  Anderson, John P.
;    TITLE OF INVENTION:  Beta-Secretase
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
```

```
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94105
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/480,498
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Heslin, James M.
;       REGISTRATION NUMBER:  29,541
;       REFERENCE/DOCKET NUMBER:  015270-002200
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-326-2400
;       TELEFAX:  415-326-2422
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-480-498-2

  Query Match             100.0%;  Score 20;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          2 NLDA 5


RESULT 5
US-08-659-984A-14
; Sequence 14, Application US/08659984A
; Patent No. 5942400
;  GENERAL INFORMATION:
;     APPLICANT:  Anderson, John P.
;     APPLICANT:  Sinha, Sukanto
;     APPLICANT:  Jacobson-Croak, Kirsten L.
;     TITLE OF INVENTION:  Assays for Detecting Beta-Secretase
;     TITLE OF INVENTION:  Inhibition
;     NUMBER OF SEQUENCES:  21
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend and Crew LLP
;       STREET:  Two Embarcadero Ctr., 8th Floor
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94111-3834
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
```

```
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/659,984A
;       FILING DATE:  07-JUN-1996
;       CLASSIFICATION:  436
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/485,152
;       FILING DATE:  07-JUN-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Heslin, James M.
;       REGISTRATION NUMBER:  29,541
;       REFERENCE/DOCKET NUMBER:  15270-002810US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-326-2400
;       TELEFAX:  415-326-2422
;   INFORMATION FOR SEQ ID NO:  14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-659-984A-14

  Query Match             100.0%;  Score 20;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          2 NLDA 5


RESULT 6
US-08-660-531-14
; Sequence 14, Application US/08660531
; Patent No. 6221645
;  GENERAL INFORMATION:
;     APPLICANT:  Chrysler, Susanna M.S.
;     APPLICANT:  Sinha, Sukanto
;     APPLICANT:  Keim, Pamela S.
;     APPLICANT:  Anderson, John P.
;     TITLE OF INVENTION:  Beta-Secretase
;     NUMBER OF SEQUENCES:  21
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend and Crew LLP
;       STREET:  Two Embarcadero Ctr., 8th Floor
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94111-3834
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
```

```
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/660,531
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/480,498
;       FILING DATE:  07-JUN-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Heslin, James M.
;       REGISTRATION NUMBER:  29,541
;       REFERENCE/DOCKET NUMBER:  15270-002210US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-326-2400
;       TELEFAX:  415-326-2422
;   INFORMATION FOR SEQ ID NO:  14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-660-531-14

  Query Match             100.0%;  Score 20;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          2 NLDA 5


RESULT 7
US-09-054-334-2
; Sequence 2, Application US/09054334
; Patent No. 6329163
;  GENERAL INFORMATION:
;     APPLICANT:  Anderson, John P.
;     APPLICANT:  Jacobson-Croak, Kirsten L.
;     APPLICANT:  Sinha, Sukanto
;     TITLE OF INVENTION:  Assays for Detecting Beta-Secretase
;     TITLE OF INVENTION:  Inhibition
;     NUMBER OF SEQUENCES:  6
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend and Crew LLP
;       STREET:  Two Embarcader Center, Eighth Floor
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94111-3834
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
```

```
;       APPLICATION NUMBER:  US/09/054,334
;       FILING DATE:  02-APR-1998
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/485,152
;       FILING DATE:  07-JUN-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Heslin, James M.
;       REGISTRATION NUMBER:  29,541
;       REFERENCE/DOCKET NUMBER:  015270-002820US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 576-0200
;       TELEFAX:  (415) 576-0300
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-09-054-334-2

  Query Match             100.0%;  Score 20;  DB 4;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          2 NLDA 5


RESULT 8
US-08-802-981-219
; Sequence 219, Application US/08802981
; Patent No. 6037137
;  GENERAL INFORMATION:
;     APPLICANT:  Komoriya, Akira
;     APPLICANT:  Packard, Beverly S.
;     TITLE OF INVENTION:  Compositions for the Detection of Enzyme
;     TITLE OF INVENTION:  Activity in Biological Samples and Methods of Use
Thereof
;     NUMBER OF SEQUENCES:  231
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend and Crew LLP
;       STREET:  Two Embarcadero Center, Eighth Floor
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94111-3834
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/802,981
;       FILING DATE:  20-FEB-1997
```

```
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Hunter, Tom
;       REGISTRATION NUMBER:  38,498
;       REFERENCE/DOCKET NUMBER:  016865-000300US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 576-0200
;       TELEFAX:  (415) 576-0300
;   INFORMATION FOR SEQ ID NO:  219:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  9 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-802-981-219

  Query Match             100.0%;  Score 20;  DB 3;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          4 NLDA 7


RESULT 9
US-08-659-984A-19
; Sequence 19, Application US/08659984A
; Patent No. 5942400
;  GENERAL INFORMATION:
;     APPLICANT:  Anderson, John P.
;     APPLICANT:  Sinha, Sukanto
;     APPLICANT:  Jacobson-Croak, Kirsten L.
;     TITLE OF INVENTION:  Assays for Detecting Beta-Secretase
;     TITLE OF INVENTION:  Inhibition
;     NUMBER OF SEQUENCES:  21
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend and Crew LLP
;       STREET:  Two Embarcadero Ctr., 8th Floor
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94111-3834
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/659,984A
;       FILING DATE:  07-JUN-1996
;       CLASSIFICATION:  436
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/485,152
;       FILING DATE:  07-JUN-1995
;     ATTORNEY/AGENT INFORMATION:
```

```
;       NAME:  Heslin, James M.
;       REGISTRATION NUMBER:  29,541
;       REFERENCE/DOCKET NUMBER:  15270-002810US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-326-2400
;       TELEFAX:  415-326-2422
;   INFORMATION FOR SEQ ID NO:  19:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;       NAME/KEY:  Region
;       LOCATION:  one-of(1)
;       OTHER INFORMATION:  /note= "N-terminal Ser is acetylated."
US-08-659-984A-19

  Query Match             100.0%;  Score 20;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          4 NLDA 7


RESULT 10
US-08-660-531-19
; Sequence 19, Application US/08660531
; Patent No. 6221645
;  GENERAL INFORMATION:
;     APPLICANT:  Chrysler, Susanna M.S.
;     APPLICANT:  Sinha, Sukanto
;     APPLICANT:  Keim, Pamela S.
;     APPLICANT:  Anderson, John P.
;     TITLE OF INVENTION:  Beta-Secretase
;     NUMBER OF SEQUENCES:  21
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend and Crew LLP
;       STREET:  Two Embarcadero Ctr., 8th Floor
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94111-3834
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/660,531
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/480,498
```

```
;       FILING DATE:  07-JUN-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Heslin, James M.
;       REGISTRATION NUMBER:  29,541
;       REFERENCE/DOCKET NUMBER:  15270-002210US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-326-2400
;       TELEFAX:  415-326-2422
;   INFORMATION FOR SEQ ID NO:  19:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;       NAME/KEY:  Region
;       LOCATION:  one-of(1)
;       OTHER INFORMATION:  /note= "N-terminal Ser is acetylated."
US-08-660-531-19

  Query Match             100.0%;  Score 20;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          4 NLDA 7


RESULT 11
US-09-548-372D-63
; Sequence 63, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280I
;  CURRENT APPLICATION NUMBER: US/09/548,372D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
```

```
;   OTHER INFORMATION: Synthetic peptide
US-09-548-372D-63

  Query Match             100.0%;  Score 20;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          4 NLDA 7


RESULT 12
US-09-548-367D-63
; Sequence 63, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
US-09-548-367D-63

  Query Match             100.0%;  Score 20;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          4 NLDA 7


RESULT 13
US-09-551-853D-63
; Sequence 63, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
```

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-551-853D-63

Query Match 100.0%; Score 20; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLDA 4
||||
Db 4 NLDA 7

RESULT 14
US-09-604-608-5
; Sequence 5, Application US/09604608
; Patent No. 6545127
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/604,608
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/141,363
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31

```
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-09-604-608-5

  Query Match             100.0%;  Score 20;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          4 NLDA 7


RESULT 15
PCT-US94-07043A-3
; Sequence 3, Application PC/TUS9407043A
;  GENERAL INFORMATION:
;    APPLICANT:  Tamburini, Paul P.; Benz, G nter; H bich,
;    APPLICANT:  Dieter; Dreyer, Robert N.; Koenig, Gerhard
;    TITLE OF INVENTION:  CATHEPSIN D IS AN AMYLOIDOGENIC
;    TITLE OF INVENTION:  PROTEASE IN ALZHEIMER S DISEASE
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miles Inc.
;      STREET:  400 Morgan Lane
;      CITY:  West Haven
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06516
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 800 kb storage
;      COMPUTER:  Sharp PC 4600
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/07043A
;      FILING DATE:  June 21, 1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/10889
;      FILING DATE:  November 12, 1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/995,660
;      FILING DATE:  December 16, 1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/880,914
;      FILING DATE:  May 11, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pamela A. Simonton
;      REGISTRATION NUMBER:  31,060
;      REFERENCE/DOCKET NUMBER:  MTI 224.3
```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 937-2340
; TELEFAX: (203) 937-2795
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US94-07043A-3

Query Match 100.0%; Score 20; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 NLDA 4
              ||||
Db          5 NLDA 8
```

Search completed: January 21, 2004, 09:27:08
Job time : 1.35946 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 21, 2004, 09:16:55 ; Search time 0.367113 Seconds
(without alignments)
1047.838 Million cell updates/sec

Title: US-09-869-414A-66
Perfect score: 20
Sequence: 1 NLDA 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	53	2	S43965	hypothetical prote
2	20	100.0	54	2	C72809	gp87 protein - Myc
3	20	100.0	68	2	A88030	protein F46F5.8 [i
4	20	100.0	70	2	S58932	DNA-directed RNA p
5	20	100.0	72	2	C89933	hypothetical prote
6	20	100.0	73	2	H90802	hypothetical prote
7	20	100.0	75	1	BVECRY	traY protein - Esc
8	20	100.0	75	2	H81320	small hydrophobic
9	20	100.0	82	2	JC4205	hypothetical 9.1k
10	20	100.0	82	2	T09234	hypothetical prote
11	20	100.0	85	1	GDEC	glutaredoxin 1 - E
12	20	100.0	85	2	A99745	hypothetical prote
13	20	100.0	85	2	E85595	hypothetical prote

14	20	100.0	88	2	A38085	S-layer glycoprote
15	20	100.0	89	2	E97731	hypothetical prote
16	20	100.0	90	1	S01373	ribonuclease inhib
17	20	100.0	91	1	C69973	ribonuclease inhib
18	20	100.0	91	2	A97004	barstar-like prote
19	20	100.0	91	2	A55406	calgranulin c - pi
20	20	100.0	93	2	AB0449	probable ribonucle
21	20	100.0	95	2	A81176	ribonuclease inhib
22	20	100.0	96	2	A57483	3-mercaptopyruvate
23	20	100.0	102	2	C84003	exogenous DNA-bind
24	20	100.0	103	2	A85821	unknown protein en
25	20	100.0	103	2	E90973	hypothetical prote
26	20	100.0	103	2	E72664	hypothetical prote
27	20	100.0	109	2	S50356	sugar transport pr
28	20	100.0	110	2	S65003	hypothetical prote
29	20	100.0	112	2	A75544	conserved hypothet
30	20	100.0	114	2	AF0252	conserved hypothet
31	20	100.0	114	2	AG0725	conserved hypothet
32	20	100.0	114	2	H89785	hypothetical prote
33	20	100.0	115	2	D32227	hypothetical prote
34	20	100.0	116	2	T44504	merP protein [impo
35	20	100.0	116	2	T45512	probable transport
36	20	100.0	116	2	C64562	hypothetical prote
37	20	100.0	119	2	F83714	holo-(acyl carrier
38	20	100.0	123	2	S55326	pseudoazurin - Thi
39	20	100.0	125	2	C98286	hypothetical prote
40	20	100.0	126	2	S53340	CD59 protein - rat
41	20	100.0	126	2	T18655	hypothetical prote
42	20	100.0	126	2	AH1425	hypothetical secre
43	20	100.0	127	2	AG1425	hypothetical secre
44	20	100.0	129	2	AE1933	hypothetical prote
45	20	100.0	129	2	AC0782	probable DNA-bindi

ALIGNMENTS

RESULT 1
S43965
hypothetical protein (clone pRK21) - Rhizobium sp. (strain NGR234) (fragment)
C;Species: Rhizobium sp.
A;Variety: strain NGR234
C;Date: 20-Oct-1994 #sequence_revision 23-Feb-1996 #text_change 02-Jul-1998
C;Accession: S43965
R;Perret, X.; Fellay, R.; Bjourson, A.J.; Cooper, J.E.; Brenner, S.; Broughton, W.J.
Nucleic Acids Res. 22, 1335-1341, 1994
A;Title: Subtraction hybridisation and shot-gun sequencing: a new approach to identify symbiotic loci.
A;Reference number: S43961; MUID:94248027; PMID:8190622
A;Accession: S43965
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-53 <PER>
A;Experimental source: strain NGR234
C;Superfamily: inner membrane protein malK; ATP-binding cassette homology
C;Keywords: ATP

F;1-53/Domain: ATP-binding cassette homology (fragment) <ABC>

  Query Match 100.0%; Score 20; DB 2; Length 53;
  Best Local Similarity 100.0%; Pred. No. 1.4e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 NLDA 4
              ||||
Db         35 NLDA 38
```

RESULT 2
C72809
gp87 protein - Mycobacterium phage D29
C;Species: Mycobacterium phage D29
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 20-Apr-2001
C;Accession: C72809
R;Ford, M.E.; Sarkis, G.J.; Belanger, A.E.; Hendrix, R.W.; Hatfull, G.F.
J. Mol. Biol. 279, 143-164, 1998
A;Title: Genome structure of mycobacteriophage D29: Implications for phage evolution.
A;Reference number: A72800; MUID:98300335; PMID:9636706
A;Accession: C72809
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-54 <FOR>
A;Cross-references: GB:AF022214; NID:g3172250; PIDN:AAC18517.1; PID:g3172324
C;Genetics:
A;Gene: 87

  Query Match 100.0%; Score 20; DB 2; Length 54;
  Best Local Similarity 100.0%; Pred. No. 1.5e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 NLDA 4
              ||||
Db          9 NLDA 12
```

RESULT 3
A88030
protein F46F5.8 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: A88030
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology.
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ for a list of authors
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 285, 1493, 1999
A;Accession: A88030
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-68 <STO>
A;Cross-references: GB:chr_II; PIDN:AC78187.1; PID:g3886036; GSPDB:GN00020;
CESP:F46F5.8
C;Genetics:
A;Gene: F46F5.8
A;Map position: 2

  Query Match   100.0%; Score 20; DB 2; Length 68;
  Best Local Similarity   100.0%; Pred. No. 1.9e+02;
  Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 NLDA 4
              ||||
Db   32 NLDA 35

RESULT 4
S58932
DNA-directed RNA polymerase (EC 2.7.7.6) chain ABC10 alpha - yeast
(Saccharomyces cerevisiae)
N;Alternate names: protein YHR143w-a; RPC10 protein
C;Species: Saccharomyces cerevisiae
C;Date: 28-Nov-1995 #sequence_revision 09-Mar-1996 #text_change 02-Jun-2000
C;Accession: S58932; S58934; S58515
R;Treich, I.; Carles, C.; Riva, M.; Sentenac, A.
Gene Expr. 2, 31-37, 1992
A;Title: RPC10 encodes a new mini subunit shared by yeast nuclear RNA
polymerases.
A;Reference number: S58932; MUID:92314714; PMID:1617300
A;Accession: S58932
A;Molecule type: DNA
A;Residues: 1-70 <TRE>
A;Cross-references: EMBL:U23378; NID:g733517; PIDN:AAA64417.1; PID:g733518
A;Accession: S58934
A;Molecule type: protein
A;Residues: 4-22;64-69 <TRW>
C;Genetics:
A;Gene: SGD:RPB12; RPC10
A;Cross-references: MIPS:YHR143w-a; SGD:S0001185
A;Map position: 8R
A;Note: YHR143w-a
C;Superfamily: DNA-directed RNA polymerase chain ABC10 alpha
C;Keywords: nucleotidyltransferase; nucleus; transcription

  Query Match   100.0%; Score 20; DB 2; Length 70;
  Best Local Similarity   100.0%; Pred. No. 1.9e+02;
  Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 NLDA 4
              ||||
Db   11 NLDA 14

RESULT 5
C89933
hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: C89933
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Aoki, K.; Nagai, Y.; Lian, J.; Ito, T.; Kanamori, M.; Matsumaru, H.; Maruyama, A.; Murakami, H.; Hosoyama, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Hirakawa, H.; Kuhara, S.; Goto, S.; Yabuzaki, J.; Kanehisa, M.; Yamashita, A.; Oshima, K.; Furuya, K.; Yoshino, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89933
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-72 <KUR>
A;Cross-references: GB:BA000018; PID:g13701330; PIDN:BAB42624.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1362

  Query Match 100.0%; Score 20; DB 2; Length 72;
  Best Local Similarity 100.0%; Pred. No. 2e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLDA 4
      ||||
Db 20 NLDA 23

RESULT 6
H90802
hypothetical protein ECs1392 [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: H90802
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Ohtsubo, E.; Nakayama, K.; Murata, T.; Tanaka, M.; Tobe, T.; Iida, T.; Takami, H.; Honda, T.; Sasakawa, C.; Ogasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H90802
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-73 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34815.1; PID:g13360852; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs1392

  Query Match 100.0%; Score 20; DB 2; Length 73;
  Best Local Similarity 100.0%; Pred. No. 2e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 NLDA 4
              ||||
Db         67 NLDA 70
```

RESULT 7
BVECRY
traY protein - Escherichia coli plasmids
C;Species: Escherichia coli
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
C;Accession: C25033; C32014
R;Finlay, B.B.; Frost, L.S.; Paranchych, W.
J. Bacteriol. 168, 132-139, 1986
A;Title: Origin of transfer of Incf plasmids and nucleotide sequences of the type II oriT, traM, and traY alleles from ColB4-K98 and the type IV traY allele from R100-1.
A;Reference number: A25033; MUID:87008371; PMID:3531163
A;Accession: C25033
A;Molecule type: DNA
A;Residues: 1-75 <FIN>
A;Cross-references: GB:M15136; NID:g151788; PIDN:AAA26076.1; PID:g151789
A;Experimental source: plasmid R100-1
R;Inamoto, S.; Yoshioka, Y.; Ohtsubo, E.
J. Bacteriol. 170, 2749-2757, 1988
A;Title: Identification and characterization of the products from the traJ and traY genes of plasmid R100.
A;Reference number: A32014; MUID:88227859; PMID:2836369
A;Accession: C32014
A;Molecule type: DNA
A;Residues: 1-75 <INA>
A;Cross-references: GB:M20941; NID:g151778; PIDN:AAA26073.1; PID:g151781
A;Experimental source: plasmid R100
C;Genetics:
A;Gene: traY
A;Genome: plasmid
A;Start codon: TTG
C;Function:
A;Description: involved in the conjugation process of bacterial cells for the exchange of plasmid DNA; also responsible for conjugal DNA metabolism
C;Superfamily: traY protein
C;Keywords: DNA binding; pilin formation; plasmid transfer

```
  Query Match             100.0%;  Score 20;  DB 1;  Length 75;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         57 NLDA 60
```

RESULT 8
H81320
small hydrophobic protein Cj1158c [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002

C;Accession: H81320
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillingworth, T.; Davies, R.M.; Feltwell, T.; Holroyd, S.; Jagels, K.; Karlyshev, A.; Moule, S.; Pallen, M.J.; Penn, C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell, B.G.
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences.
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: H81320
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-75 <PAR>
A;Cross-references: GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB73412.1; PID:g6968591; GSPDB:GN00120; CJSP:Cj1158c
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj1158c

  Query Match 100.0%; Score 20; DB 2; Length 75;
  Best Local Similarity 100.0%; Pred. No. 2.1e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLDA 4
      ||||
Db 6 NLDA 9

RESULT 9
JC4205
hypothetical 9.1k protein - Frankia sp.
C;Species: Frankia sp.
C;Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 22-Oct-1999
C;Accession: JC4205
R;Harriott, O.T.; Hosted, T.J.; Benson, D.R.
Gene 161, 63-67, 1995
A;Title: Sequences of nifX, nifW, nifZ, nifB and two ORF in the Frankia nitrogen fixation gene cluster.
A;Reference number: JC4203; MUID:95369734; PMID:7642138
A;Accession: JC4205
A;Molecule type: DNA
A;Residues: 1-82 <HAR>
A;Cross-references: GB:L29299; NID:g497430; PIDN:AAC82972.1; PID:g497433

  Query Match 100.0%; Score 20; DB 2; Length 82;
  Best Local Similarity 100.0%; Pred. No. 2.3e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLDA 4
      ||||
Db 17 NLDA 20

RESULT 10
T09234
hypothetical protein 1 - Frankia alni
C;Species: Frankia alni

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T09234
R;Benson, D.R.
submitted to the EMBL Data Library, November 1998
A;Reference number: Z16624
A;Accession: T09234
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-82 <BEN>
A;Cross-references: EMBL:L29299; NID:g3953454; PID:g497433
A;Experimental source: strain cpI1

  Query Match   100.0%; Score 20; DB 2; Length 82;
  Best Local Similarity   100.0%; Pred. No. 2.3e+02;
  Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 NLDA 4
              ||||
Db   17 NLDA 20

RESULT 11
GDEC
glutaredoxin 1 - Escherichia coli (strain K-12)
N;Alternate names: thioltransferase
C;Species: Escherichia coli
C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 01-Mar-2002
C;Accession: A00283; A24397; I59418; A64823; A39568
R;Hoeoeg, J.O.; Joernvall, H.; Holmgren, A.; Carlquist, M.; Persson, M.
Eur. J. Biochem. 136, 223-232, 1983
A;Title: The primary structure of Escherichia coli glutaredoxin. Distant
homology with thioredoxins in a superfamily of small proteins with a redox-
active cystine disulfide/cysteine dithiol.
A;Reference number: A00283; MUID:84004402; PMID:6352262
A;Accession: A00283
A;Molecule type: protein
A;Residues: 1-85 <HO1>
A;Experimental source: K-12, strain C10-17
R;Hoeoeg, J.O.; von Bahr-Lindstroem, H.; Joernvall, H.; Holmgren, A.
Gene 43, 13-21, 1986
A;Title: Cloning and expression of the glutaredoxin (grx) gene of Escherichia
coli.
A;Reference number: A24397; MUID:87005940; PMID:3530878
A;Accession: A24397
A;Molecule type: DNA
A;Residues: 1-85 <HO2>
A;Cross-references: GB:M13449; NID:g146272; PIDN:AAA23936.1; PID:g146273
R;Chatterjee, P.K.; Sternberg, N.L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8950-8954, 1995
A;Title: A general genetic approach in Escherichia coli for determining the
mechanism(s) of action of tumoricidal agents: application to DMP 840, a
tumoricidal agent.
A;Reference number: I59418; MUID:96004656; PMID:7568050
A;Accession: I59418
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-85 <RES>

A;Cross-references: EMBL:U18655; NID:g609323; PIDN:AAC43449.1; PID:g609325
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A64823
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-85 <BLAT>
A;Cross-references: GB:AE000187; GB:U00096; NID:g1787070; PIDN:AAC73936.1; PID:g1787073; UWGP:b0849
A;Experimental source: strain K-12, substrain MG1655
R;Sandberg, V.A.; Kren, B.; Fuchs, J.A.; Woodward, C.
Biochemistry 30, 5475-5484, 1991
A;Title: Escherichia coli glutaredoxin: cloning and overexpression, thermodynamic stability of the oxidized and reduced forms, and report of an N-terminal extended species.
A;Reference number: A39568; MUID:91242463; PMID:2036416
A;Accession: A39568
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 'MRREI',1-15 <SAN>
C;Genetics:
A;Gene: grxA; grx
A;Map position: 19 min
C;Function:
A;Description: the disulfide bond functions as an electron carrier in the glutathione-dependent synthesis of deoxyribonucleotides from ribonucleotides by the enzyme ribonucleotide reductase; in addition, it is also involved in reducing some disulfides in a coupled system with glutathione reductase
A;Pathway: deoxyribonucleotide biosynthesis
C;Superfamily: glutaredoxin; glutaredoxin homology
C;Keywords: deoxyribonucleotide biosynthesis; electron transfer; monomer; redox-active disulfide
F;1-85/Domain: glutaredoxin homology <GLUT>
F;11-14/Disulfide bonds: redox-active #status experimental

  Query Match 100.0%; Score 20; DB 1; Length 85;
  Best Local Similarity 100.0%; Pred. No. 2.4e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 NLDA 4
              ||||
Db         82 NLDA 85
```

RESULT 12
A99745
hypothetical protein ECs0929 [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 30-Jun-2002
C;Accession: A99745
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Ohtsubo, E.; Nakayama, K.; Murata, T.; Tanaka, M.; Tobe, T.; Iida,

T.; Takami, H.; Honda, T.; Sasakawa, C.; Ogasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A99745
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-85 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34352.1; PID:g13360388; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0929
C;Superfamily: glutaredoxin; glutaredoxin homology
C;Keywords: redox-active disulfide
F;11-14/Disulfide bonds: redox-active #status predicted

  Query Match 100.0%; Score 20; DB 2; Length 85;
  Best Local Similarity 100.0%; Pred. No. 2.4e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLDA 4
      ||||
Db 82 NLDA 85

RESULT 13
E85595
hypothetical protein grxA [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 30-Jun-2002
C;Accession: E85595
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, G.F.; Evans, P.S.; Gregor, J.; Kirkpatrick, H.A.; Posfai, G.; Hackett, J.; Klink, S.; Boutin, A.; Shao, Y.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, J.; Anantharaman, T.S.; Lin, J.; Yen, G.; Schwartz, D.C.; Welch, R.A.; Blattner, F.R.
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E85595
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-85 <STO>
A;Cross-references: GB:AE005174; NID:g12513864; PIDN:AAG55225.1; GSPDB:GN00145; UWGP:Z1076
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: grxA
C;Superfamily: glutaredoxin; glutaredoxin homology
C;Keywords: redox-active disulfide
F;11-14/Disulfide bonds: redox-active #status predicted

  Query Match 100.0%; Score 20; DB 2; Length 85;
  Best Local Similarity 100.0%; Pred. No. 2.4e+02;

```
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         82 NLDA 85


RESULT 14
A38085
S-layer glycoprotein - Haloferax volcanii (fragments)
C;Species: Haloferax volcanii
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 04-Sep-1998
C;Accession: A38085
R;Mengele, R.; Sumper, M.
J. Biol. Chem. 267, 8182-8185, 1992
A;Title: Drastic differences in glycosylation of related S-layer glycoproteins
from moderate and extreme halophiles.
A;Reference number: A38085; MUID:92235030; PMID:1569073
A;Accession: A38085
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-88 <MEN>
C;Superfamily: S-layer glycoprotein
C;Keywords: glycoprotein

  Query Match             100.0%;  Score 20;  DB 2;  Length 88;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          2 NLDA 5


RESULT 15
E97731
hypothetical protein RC0253 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C;Accession: E97731
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.;
Samson, D.; Roux, V.; Cossart, P.; Weissenbach, J.; Claverie, J.M.; Raoult, D.
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia
prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: E97731
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-89 <KUR>
A;Cross-references: GB:AE006914; PIDN:AAL02791.1; PID:g15619308; GSPDB:GN00173
C;Genetics:
A;Gene: RC0253

  Query Match             100.0%;  Score 20;  DB 2;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 NLDA 4
              ||||
Db         35 NLDA 38
```

Search completed: January 21, 2004, 09:26:10
Job time : 2.36711 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 21, 2004, 09:25:15 ; Search time 0.803059 Seconds
(without alignments)
1018.511 Million cell updates/sec

Title: US-09-869-414A-66
Perfect score: 20
Sequence: 1 NLDA 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 762491 seqs, 204481190 residues

Total number of hits satisfying chosen parameters: 762491

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	20	100.0	4	9	US-09-794-927-66	Sequence 66, Appl
2	20	100.0	4	9	US-09-795-847-66	Sequence 66, Appl
3	20	100.0	4	9	US-09-794-743-66	Sequence 66, Appl
4	20	100.0	4	9	US-09-794-748-66	Sequence 66, Appl
5	20	100.0	4	9	US-09-794-925-66	Sequence 66, Appl
6	20	100.0	4	9	US-09-681-442-66	Sequence 66, Appl
7	20	100.0	4	11	US-09-869-414-66	Sequence 66, Appl
8	20	100.0	4	12	US-10-427-208-2	Sequence 2, Appli
9	20	100.0	9	9	US-09-896-874-8	Sequence 8, Appli
10	20	100.0	9	10	US-09-896-139-8	Sequence 8, Appli
11	20	100.0	9	10	US-09-895-843-8	Sequence 8, Appli
12	20	100.0	9	11	US-09-895-871-8	Sequence 8, Appli
13	20	100.0	9	12	US-10-066-319-4	Sequence 4, Appli
14	20	100.0	9	12	US-10-160-777-8	Sequence 8, Appli
15	20	100.0	9	12	US-10-337-075-8	Sequence 8, Appli
16	20	100.0	9	15	US-10-192-625-8	Sequence 8, Appli
17	20	100.0	9	15	US-10-192-424-8	Sequence 8, Appli
18	20	100.0	9	15	US-10-183-126A-8	Sequence 8, Appli
19	20	100.0	9	15	US-10-171-343-8	Sequence 8, Appli
20	20	100.0	9	15	US-10-264-707-8	Sequence 8, Appli
21	20	100.0	10	9	US-09-794-927-63	Sequence 63, Appl
22	20	100.0	10	9	US-09-795-847-63	Sequence 63, Appl
23	20	100.0	10	9	US-09-794-743-63	Sequence 63, Appl
24	20	100.0	10	9	US-09-794-748-63	Sequence 63, Appl
25	20	100.0	10	9	US-09-796-264-5	Sequence 5, Appli
26	20	100.0	10	9	US-09-794-925-63	Sequence 63, Appl
27	20	100.0	10	9	US-09-681-442-63	Sequence 63, Appl
28	20	100.0	10	10	US-09-845-226-5	Sequence 5, Appli
29	20	100.0	10	10	US-09-795-903A-5	Sequence 5, Appli
30	20	100.0	10	11	US-09-869-414-63	Sequence 63, Appl
31	20	100.0	10	11	US-09-548-366-63	Sequence 63, Appl
32	20	100.0	10	12	US-10-050-200-22	Sequence 22, Appl
33	20	100.0	10	15	US-10-032-818-8	Sequence 8, Appli
34	20	100.0	11	12	US-10-354-955-2	Sequence 2, Appli
35	20	100.0	11	12	US-10-354-955-4	Sequence 4, Appli
36	20	100.0	12	9	US-09-896-874-1	Sequence 1, Appli
37	20	100.0	12	10	US-09-896-139-1	Sequence 1, Appli
38	20	100.0	12	10	US-09-895-843-1	Sequence 1, Appli
39	20	100.0	12	11	US-09-895-871-1	Sequence 1, Appli
40	20	100.0	12	15	US-10-032-818-26	Sequence 26, Appl
41	20	100.0	13	12	US-10-160-777-1	Sequence 1, Appli
42	20	100.0	13	12	US-10-337-075-1	Sequence 1, Appli
43	20	100.0	13	12	US-10-372-473-12	Sequence 12, Appl
44	20	100.0	13	15	US-10-192-625-1	Sequence 1, Appli
45	20	100.0	13	15	US-10-192-424-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-794-927-66
; Sequence 66, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-927-66

Query Match 100.0%; Score 20; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 NLDA 4
              ||||
Db          1 NLDA 4
```

RESULT 2
US-09-795-847-66
; Sequence 66, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-795-847-66

  Query Match   100.0%; Score 20; DB 9; Length 4;
  Best Local Similarity   100.0%; Pred. No. 6.7e+05;
  Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 NLDA 4
              ||||
Db   1 NLDA 4

RESULT 3
US-09-794-743-66
; Sequence 66, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73

```
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 66
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-743-66

  Query Match             100.0%;  Score 20;  DB 9;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 6.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          1 NLDA 4


RESULT 4
US-09-794-748-66
; Sequence 66, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280JL
;  CURRENT APPLICATION NUMBER: US/09/794,748
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 66
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-748-66

  Query Match             100.0%;  Score 20;  DB 9;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 6.7e+05;
```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 NLDA 4
              ||||
Db          1 NLDA 4
```

RESULT 5
US-09-794-925-66
; Sequence 66, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-925-66

Query Match 100.0%; Score 20; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 NLDA 4
              ||||
Db          1 NLDA 4
```

RESULT 6
US-09-681-442-66
; Sequence 66, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-681-442-66

Query Match 100.0%; Score 20; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLDA 4
||||
Db 1 NLDA 4

RESULT 7
US-09-869-414-66
; Sequence 66, Application US/09869414
; Publication No. US20030077226A1
; GENERAL INFORMATION:
; APPLICANT: Beinkowski et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280M
; CURRENT APPLICATION NUMBER: US/09/869,414
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-869-414-66

  Query Match   100.0%; Score 20; DB 11; Length 4;
  Best Local Similarity   100.0%; Pred. No. 6.7e+05;
  Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 NLDA 4
              ||||
Db   1 NLDA 4

RESULT 8
US-10-427-208-2
; Sequence 2, Application US/10427208
; Publication No. US20030200555A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Hazuda, Daria J
; APPLICANT: Chen Dodson, Elizabeth
; APPLICANT: Lai, Ming-Tain
; APPLICANT: Xu, Min
; APPLICANT: Shi, Xiao-Ping
; APPLICANT: Simon, Adam J.
; APPLICANT: Wu, Guoxin
; APPLICANT: Li, Yueming
; APPLICANT: Register, Robert B.
; TITLE OF INVENTION: ASSAYS USING AMYLOID PRECURSOR PROTEINS WITH MODIFIED
; TITLE OF INVENTION: BETA-SECRETASE CLEAVAGE SITES TO MONITOR BETA-SECRETASE
ACTIVITY
; FILE REFERENCE: 21052
; CURRENT APPLICATION NUMBER: US/10/427,208
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-427-208-2

  Query Match   100.0%; Score 20; DB 12; Length 4;
  Best Local Similarity   100.0%; Pred. No. 6.7e+05;
  Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 NLDA 4
              ||||
Db          1 NLDA 4


RESULT 9
US-09-896-874-8
; Sequence 8, Application US/09896874
; Patent No. US20020016320A1
; GENERAL INFORMATION:
;  APPLICANT: Fang, Lawrence Y.
;  APPLICANT:  John, Varghese
;  TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
;  FILE REFERENCE: 13615.40USU1
;  CURRENT APPLICATION NUMBER: US/09/896,874
;  CURRENT FILING DATE:  2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/215,323
;  PRIOR FILING DATE: 2000-06-30
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-896-874-8

  Query Match             100.0%;  Score 20;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 6.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          4 NLDA 7


RESULT 10
US-09-896-139-8
; Sequence 8, Application US/09896139
; Patent No. US20020128255A1
; GENERAL INFORMATION:
;  APPLICANT: Beck, James P.
;  APPLICANT:  Fang, Lawrence Y.
;  APPLICANT:  Freskos, John N.
;  APPLICANT:  Gailunas, Andrea
;  APPLICANT:  Hom, Roy
;  APPLICANT:  Jagodizinska, Barbara
;  APPLICANT:  John, Varghese
;  APPLICANT:  Maillaird, Michel
;  APPLICANT:  Pulley, Shon R.
;  APPLICANT:  TenBrink, Ruth E.
;  TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
;  FILE REFERENCE: 13615.25USU4
;  CURRENT APPLICATION NUMBER: US/09/896,139
;  CURRENT FILING DATE:  2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/215,323
```

; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/252,736
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/255,956
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/268,497
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: US 60/279,779
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 60/295,589
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-896-139-8

  Query Match   100.0%; Score 20; DB 10; Length 9;
  Best Local Similarity   100.0%; Pred. No. 6.7e+05;
  Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 NLDA 4
              ||||
Db   4 NLDA 7

RESULT 11
US-09-895-843-8
; Sequence 8, Application US/09895843
; Patent No. US20020143177A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John N.
; APPLICANT: Gailunas, Andrea
; APPLICANT: Hom, Roy
; APPLICANT: Jagodizinska, Barbara
; APPLICANT: John, Varghese
; APPLICANT: Maillaird, Michel
; APPLICANT: Pulley, Shon R.
; APPLICANT: TenBrink, Ruth E.
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.41USU1
; CURRENT APPLICATION NUMBER: US/09/895,843
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence

```
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-895-843-8

  Query Match             100.0%;  Score 20;  DB 10;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 6.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          4 NLDA 7


RESULT 12
US-09-895-871-8
; Sequence 8, Application US/09895871
; Publication No. US20030096864A1
; GENERAL INFORMATION:
;  APPLICANT: Fang, Lawrence Y.
;  APPLICANT:  Hom, Roy
;  APPLICANT:  John, Varghese
;  APPLICANT:  Maillaird, Michel
;  TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
;  FILE REFERENCE: 13615.21USU1
;  CURRENT APPLICATION NUMBER: US/09/895,871
;  CURRENT FILING DATE:  2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/215,323
;  PRIOR FILING DATE: 2000-06-30
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-895-871-8

  Query Match             100.0%;  Score 20;  DB 11;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 6.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          4 NLDA 7


RESULT 13
US-10-066-319-4
; Sequence 4, Application US/10066319
; Publication No. US20030147810A1
; GENERAL INFORMATION:
;  APPLICANT: Ross, Brian D.
;  APPLICANT:  Rehemtulla, Alnawaz
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REPORTING
;  TITLE OF INVENTION:  OF PROTEASE ACTIVITY WITHIN THE SECRETORY PATHWAY
;  FILE REFERENCE: 11203-007001
```

```
;  CURRENT APPLICATION NUMBER: US/10/066,319
;  CURRENT FILING DATE:  2002-06-17
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-066-319-4

  Query Match             100.0%;  Score 20;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 6.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          4 NLDA 7


RESULT 14
US-10-160-777-8
; Sequence 8, Application US/10160777
; Publication No. US20030166717A1
; GENERAL INFORMATION:
;  APPLICANT: Freskos, John
;  APPLICANT:  Brown, David L.
;  APPLICANT:  Fobian, Yvette M.
;  APPLICANT:  Fang, Larry
;  APPLICANT:  Romero, Arthur G.
;  APPLICANT:  Varghese, John
;  TITLE OF INVENTION: Hydroxy Alkyl Amines
;  FILE REFERENCE: 01-1632-C
;  CURRENT APPLICATION NUMBER: US/10/160,777
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/343,772
;  PRIOR FILING DATE: 2001-12-28
;  PRIOR APPLICATION NUMBER: 60/332,639
;  PRIOR FILING DATE: 2001-11-19
;  PRIOR APPLICATION NUMBER: 60/295,332
;  PRIOR FILING DATE: 2001-06-01
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic peptide
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: N-terminal biotin
US-10-160-777-8

  Query Match             100.0%;  Score 20;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 6.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 NLDA 4
              ||||
Db          4 NLDA 7


RESULT 15
US-10-337-075-8
; Sequence 8, Application US/10337075
; Publication No. US20030166580A1
; GENERAL INFORMATION:
;  APPLICANT: Warpehoski, Martha A.
;  APPLICANT:  Jagodzinska, Barbara
;  TITLE OF INVENTION: Substituted Amino Carboxamides for the Treatment of
Alzheimer's Disease
;  FILE REFERENCE: 01-1795-C
;  CURRENT APPLICATION NUMBER: US/10/337,075
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: 60/345,316
;  PRIOR FILING DATE: 2002-01-04
;  PRIOR APPLICATION NUMBER: 60/350,419
;  PRIOR FILING DATE: 2002-01-18
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic peptide
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: N-terminal biotin
US-10-337-075-8

  Query Match             100.0%;  Score 20;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 6.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          4 NLDA 7


Search completed: January 21, 2004, 09:41:42
Job time : 0.803059 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 21, 2004, 09:16:19 ; Search time 0.826004 Seconds
(without alignments)
1249.644 Million cell updates/sec

Title: US-09-869-414A-66
Perfect score: 20
Sequence: 1 NLDA 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	20	100.0	26	5	Q9BM03	Q9bm03 dugesia tig
2	20	100.0	33	5	Q9GTB2	Q9gtb2 eimeria ten
3	20	100.0	33	5	Q9GTC2	Q9gtc2 plasmodium
4	20	100.0	33	5	Q9GTA9	Q9gta9 sarcocystis
5	20	100.0	33	5	Q9GT95	Q9gt95 cryptospori
6	20	100.0	33	5	Q9GTA2	Q9gta2 babesia bov
7	20	100.0	41	6	Q9N194	Q9n194 macaca mula
8	20	100.0	41	6	Q9N191	Q9n191 hylobates l
9	20	100.0	41	6	Q9N193	Q9n193 gorilla gor
10	20	100.0	41	6	Q9N192	Q9n192 pan troglod
11	20	100.0	41	16	Q8PGA4	Q8pga4 xanthomonas
12	20	100.0	42	2	Q53299	Q53299 escherichia
13	20	100.0	42	15	Q9Q582	Q9q582 human immun
14	20	100.0	50	2	Q8KM85	Q8km85 mycoplasma
15	20	100.0	50	5	Q8T642	Q8t642 ceratitis c
16	20	100.0	50	5	Q8T643	Q8t643 ceratitis c
17	20	100.0	51	16	Q8RAW6	Q8raw6 thermoanaer
18	20	100.0	54	16	Q99ZY5	Q99zy5 streptococc
19	20	100.0	54	16	Q8P193	Q8p193 streptococc
20	20	100.0	55	16	Q8CKW2	Q8ckw2 yersinia pe
21	20	100.0	57	12	Q91TH0	Q91th0 tupaia herp
22	20	100.0	59	10	Q8GRR3	Q8grr3 oryza sativ
23	20	100.0	66	3	Q96X11	Q96x11 phaeosphaer
24	20	100.0	68	5	Q9TXY3	Q9txy3 caenorhabdi
25	20	100.0	69	12	Q8VAI7	Q8vai7 white spot
26	20	100.0	69	16	Q8DFY4	Q8dfy4 vibrio vuln
27	20	100.0	71	2	Q93PT2	Q93pt2 lactococcus
28	20	100.0	72	16	Q99TW2	Q99tw2 staphylococ
29	20	100.0	72	16	Q8NWD2	Q8nwd2 staphylococ
30	20	100.0	72	16	Q8K7S9	Q8k7s9 streptococc
31	20	100.0	73	4	O95641	O95641 homo sapien
32	20	100.0	73	16	Q8X2G0	Q8x2g0 escherichia
33	20	100.0	75	16	Q9PND7	Q9pnd7 campylobact
34	20	100.0	75	16	Q8XVB9	Q8xvb9 ralstonia s
35	20	100.0	80	5	Q8T640	Q8t640 apis mellif
36	20	100.0	83	10	Q9AXX2	Q9axx2 brassica na
37	20	100.0	85	10	Q9AXX0	Q9axx0 brassica ca
38	20	100.0	85	16	Q8X6S5	Q8x6s5 escherichia
39	20	100.0	86	5	Q8T641	Q8t641 manduca sex
40	20	100.0	88	2	Q9X5H7	Q9x5h7 helicobacte
41	20	100.0	89	2	Q9AKH6	Q9akh6 rickettsia
42	20	100.0	89	16	Q92J16	Q92j16 rickettsia
43	20	100.0	90	16	Q8FJF3	Q8fjf3 escherichia
44	20	100.0	91	4	Q9H4V4	Q9h4v4 homo sapien
45	20	100.0	91	16	O07938	O07938 bacillus su

ALIGNMENTS

RESULT 1
Q9BM03
ID Q9BM03 PRELIMINARY; PRT; 26 AA.
AC Q9BM03;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

```
DE   Mariner-like transposase (Fragment).
OS   Dugesia tigrina (Planarian).
OC   Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC   Paludicola; Dugesiidae; Girardia.
OX   NCBI_TaxID=6162;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TRANSPOSON=marM1;
RX   MEDLINE=20570504; PubMed=11121049;
RA   Arkhipova I., Meselson M.;
RT   "Transposable elements in sexual and ancient asexual taxa.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:14473-14477(2000).
DR   EMBL; AY014003; AAG59975.1; -.
FT   NON_TER       1      1
FT   NON_TER      26     26
SQ   SEQUENCE   26 AA;  2946 MW;  74D1AD8CA4ADA347 CRC64;

  Query Match             100.0%;  Score 20;  DB 5;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         15 NLDA 18


RESULT 2
Q9GTB2
ID   Q9GTB2      PRELIMINARY;      PRT;    33 AA.
AC   Q9GTB2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin E (Fragment).
OS   Eimeria tenella.
OC   Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
OC   Eimeria.
OX   NCBI_TaxID=5802;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21215633; PubMed=11318578;
RA   Heintzelman M.B., Schwartzman J.D.;
RT   "Myosin diversity in Apicomplexa.";
RL   J. Parasitol. 87:429-432(2001).
DR   EMBL; AF273855; AAG29117.1; -.
DR   InterPro; IPR001609; myosin_head.
DR   ProDom; PD000355; myosin_head; 1.
FT   NON_TER       1      1
FT   NON_TER      33     33
SQ   SEQUENCE   33 AA;  3638 MW;  2E0CFB42104F2290 CRC64;

  Query Match             100.0%;  Score 20;  DB 5;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
```

```
Db         17 NLDA 20


RESULT 3
Q9GTC2
ID   Q9GTC2      PRELIMINARY;      PRT;    33 AA.
AC   Q9GTC2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin D (Fragment).
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21215633; PubMed=11318578;
RA   Heintzelman M.B., Schwartzman J.D.;
RT   "Myosin diversity in Apicomplexa.";
RL   J. Parasitol. 87:429-432(2001).
DR   EMBL; AF273845; AAG29107.1; -.
DR   InterPro; IPR001609; myosin_head.
DR   ProDom; PD000355; myosin_head; 1.
FT   NON_TER       1      1
FT   NON_TER      33     33
SQ   SEQUENCE   33 AA;  3638 MW;  2E0CFB42104F2290 CRC64;

  Query Match             100.0%;  Score 20;  DB 5;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         17 NLDA 20


RESULT 4
Q9GTA9
ID   Q9GTA9      PRELIMINARY;      PRT;    33 AA.
AC   Q9GTA9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin B (Fragment).
OS   Sarcocystis muris.
OC   Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC   Sarcocystis.
OX   NCBI_TaxID=5813;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21215633; PubMed=11318578;
RA   Heintzelman M.B., Schwartzman J.D.;
RT   "Myosin diversity in Apicomplexa.";
RL   J. Parasitol. 87:429-432(2001).
DR   EMBL; AF273858; AAG29120.1; -.
DR   InterPro; IPR001609; myosin_head.
DR   ProDom; PD000355; myosin_head; 1.
```

```
FT   NON_TER       1      1
FT   NON_TER      33     33
SQ   SEQUENCE   33 AA;  3638 MW;  2E0CFB42104F2290 CRC64;

  Query Match             100.0%;  Score 20;  DB 5;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         17 NLDA 20


RESULT 5
Q9GT95
ID   Q9GT95      PRELIMINARY;      PRT;    33 AA.
AC   Q9GT95;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin D (Fragment).
OS   Cryptosporidium parvum.
OC   Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC   Cryptosporidiidae; Cryptosporidium.
OX   NCBI_TaxID=5807;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21215633; PubMed=11318578;
RA   Heintzelman M.B., Schwartzman J.D.;
RT   "Myosin diversity in Apicomplexa.";
RL   J. Parasitol. 87:429-432(2001).
DR   EMBL; AF273872; AAG29134.1; -.
DR   InterPro; IPR001609; myosin_head.
DR   ProDom; PD000355; myosin_head; 1.
FT   NON_TER       1      1
FT   NON_TER      33     33
SQ   SEQUENCE   33 AA;  3638 MW;  2E0CFB42104F2290 CRC64;

  Query Match             100.0%;  Score 20;  DB 5;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         17 NLDA 20


RESULT 6
Q9GTA2
ID   Q9GTA2      PRELIMINARY;      PRT;    33 AA.
AC   Q9GTA2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin D (Fragment).
OS   Babesia bovis.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
```

```
OX   NCBI_TaxID=5865;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21215633; PubMed=11318578;
RA   Heintzelman M.B., Schwartzman J.D.;
RT   "Myosin diversity in Apicomplexa.";
RL   J. Parasitol. 87:429-432(2001).
DR   EMBL; AF273865; AAG29127.1; -.
DR   InterPro; IPR001609; myosin_head.
DR   ProDom; PD000355; myosin_head; 1.
FT   NON_TER       1      1
FT   NON_TER      33     33
SQ   SEQUENCE   33 AA;  3638 MW;  2E0CFB42104F2290 CRC64;

  Query Match             100.0%;  Score 20;  DB 5;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         17 NLDA 20


RESULT 7
Q9N194
ID   Q9N194      PRELIMINARY;      PRT;    41 AA.
AC   Q9N194;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Soluble guanylyl cyclase subunit beta 2 (Fragment).
GN   GUCY1B2.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20241821; PubMed=10777682;
RA   Behrends S., Vehse K.;
RT   "The beta(2) Subunit of Soluble Guanylyl Cyclase Contains a Human-
RT   Specific Frameshift and Is Expressed in Gastric Carcinoma.";
RL   Biochem. Biophys. Res. Commun. 271:64-69(2000).
DR   EMBL; AF218384; AAF66106.1; -.
FT   NON_TER       1      1
FT   NON_TER      41     41
SQ   SEQUENCE   41 AA;  4948 MW;  31ACA70C43358DC1 CRC64;

  Query Match             100.0%;  Score 20;  DB 6;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         28 NLDA 31
```

```
RESULT 8
Q9N191
ID   Q9N191      PRELIMINARY;      PRT;    41 AA.
AC   Q9N191;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   Soluble guanylyl cyclase subunit beta 2 (Fragment).
GN   GUCY1B2.
OS   Hylobates lar (Common gibbon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX   NCBI_TaxID=9580;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20241821; PubMed=10777682;
RA   Behrends S., Vehse K.;
RT   "The beta(2) Subunit of Soluble Guanylyl Cyclase Contains a Human-
RT   Specific Frameshift and Is Expressed in Gastric Carcinoma.";
RL   Biochem. Biophys. Res. Commun. 271:64-69(2000).
DR   EMBL; AF218387; AAF66109.1; -.
FT   NON_TER       1      1
FT   NON_TER      41     41
SQ   SEQUENCE   41 AA;  4847 MW;  0B9F972BFC7E6DDB CRC64;

  Query Match             100.0%;  Score 20;  DB 6;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         28 NLDA 31


RESULT 9
Q9N193
ID   Q9N193      PRELIMINARY;      PRT;    41 AA.
AC   Q9N193;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Soluble guanylyl cyclase subunit beta 2 (Fragment).
GN   GUCY1B2.
OS   Gorilla gorilla (gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9593;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20241821; PubMed=10777682;
RA   Behrends S., Vehse K.;
RT   "The beta(2) Subunit of Soluble Guanylyl Cyclase Contains a Human-
RT   Specific Frameshift and Is Expressed in Gastric Carcinoma.";
RL   Biochem. Biophys. Res. Commun. 271:64-69(2000).
DR   EMBL; AF218385; AAF66107.1; -.
FT   NON_TER       1      1
```

```
FT   NON_TER       41      41
SQ   SEQUENCE   41 AA;  4888 MW;  31ACA718FC7E6DC1 CRC64;

  Query Match             100.0%;  Score 20;  DB 6;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         28 NLDA 31


RESULT 10
Q9N192
ID   Q9N192      PRELIMINARY;      PRT;    41 AA.
AC   Q9N192;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Soluble guanylyl cyclase subunit beta 2 (Fragment).
GN   GUCY1B2.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20241821; PubMed=10777682;
RA   Behrends S., Vehse K.;
RT   "The beta(2) Subunit of Soluble Guanylyl Cyclase Contains a Human-
RT   Specific Frameshift and Is Expressed in Gastric Carcinoma.";
RL   Biochem. Biophys. Res. Commun. 271:64-69(2000).
DR   EMBL; AF218386; AAF66108.1; -.
FT   NON_TER       1       1
FT   NON_TER      41      41
SQ   SEQUENCE   41 AA;  4888 MW;  31ACA718FC7E6DC1 CRC64;

  Query Match             100.0%;  Score 20;  DB 6;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         28 NLDA 31


RESULT 11
Q8PGA4
ID   Q8PGA4      PRELIMINARY;      PRT;    41 AA.
AC   Q8PGA4;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Peptidase.
GN   XAC3713.
OS   Xanthomonas axonopodis (pv. citri).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
```

```
OC   Xanthomonadaceae; Xanthomonas.
OX   NCBI_TaxID=92829;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=306 / ATCC 13902 / XV 101;
RX   MEDLINE=22022145; PubMed=12024217;
RA   da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA   Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA   Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA   Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA   Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA   Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA   Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA   Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA   Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA   Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA   Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA   Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA   Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA   Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA   Setubal J.C., Kitajima J.P.;
RT   "Comparison of the genomes of two Xanthomonas pathogens with differing
RT   host specificities.";
RL   Nature 417:459-463(2002).
DR   EMBL; AE012021; AAM38556.1; -.
DR   InterPro; IPR000718; Peptidase_M13.
DR   Pfam; PF01431; Peptidase_M13; 1.
KW   Complete proteome.
SQ   SEQUENCE   41 AA;  4918 MW;  BD75A10CBFE67628 CRC64;

  Query Match             100.0%;  Score 20;  DB 16;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         14 NLDA 17


RESULT 12
Q53299
ID   Q53299      PRELIMINARY;      PRT;    42 AA.
AC   Q53299;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   AphA1 protein (Fragment).
GN   APHA1.
OS   Escherichia coli.
OG   Plasmid pIP1518.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93159149; PubMed=8381641;
RA   Menard R., Molinas C., Arthur M., Duval J., Courvalin P., Leclercq R.;
```

```
RT   "Overproduction of 3'-aminoglycoside phosphotransferase type I confers
RT   resistance to tobramycin in Escherichia coli.";
RL   Antimicrob. Agents Chemother. 37:78-83(1993).
DR   EMBL; S54065; AAD13871.1; -.
KW   Plasmid.
FT   NON_TER      42     42
SQ   SEQUENCE   42 AA;  4831 MW;  D6894835CE244D87 CRC64;

  Query Match             100.0%;  Score 20;  DB 2;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         18 NLDA 21


RESULT 13
Q9Q582
ID   Q9Q582      PRELIMINARY;      PRT;    42 AA.
AC   Q9Q582;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Envelope glycoprotein V2 region (Fragment).
GN   ENV.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wang B., Saksena N.K.;
RT   "HIV-1 Strains from a cohort of American subjects reveal the presence
RT   of a V2 region extension unique to slow progressors and non-
RT   progressors.";
RL   AIDS 0:0-0(2000).
DR   EMBL; AF203211; AAF24360.1; -.
DR   InterPro; IPR000777; GP120.
DR   Pfam; PF00516; GP120; 1.
KW   AIDS; Coat protein; Glycoprotein.
FT   NON_TER       1      1
FT   NON_TER      42     42
SQ   SEQUENCE   42 AA;  4790 MW;  DE78892C9F92A38B CRC64;

  Query Match             100.0%;  Score 20;  DB 15;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         22 NLDA 25


RESULT 14
Q8KM85
ID   Q8KM85      PRELIMINARY;      PRT;    50 AA.
AC   Q8KM85;
```

```
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Mycoplasma suis.
OC   Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=57372;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=54/96;
RA   Hoelzle L.E., Adelt D., Hoelzle K., Heinritzi K., Wittenbrink M.M.;
RT   "Purification and analysis of Mycoplasma suis (Eperythrozoon suis) DNA
RT   from porcine blood.";
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ504999; CAD44546.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   50 AA;  5767 MW;  93B2745C684D6547 CRC64;

  Query Match             100.0%;  Score 20;  DB 2;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         26 NLDA 29


RESULT 15
Q8T642
ID   Q8T642      PRELIMINARY;      PRT;    50 AA.
AC   Q8T642;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Integrin betaPS4B (Fragment).
OS   Ceratitis capitata (Mediterranean fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Tephritoidea; Tephritidae; Ceratitis.
OX   NCBI_TaxID=7213;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bunch T.A., Miller S.W., Brower D.L.;
RT   "Mutations in the C8-C9 loop of the Drosophila betaPS subunit affect
RT   integrin regulation.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF487331; AAL93260.1; -.
DR   InterPro; IPR002369; Integrin_B.
DR   Pfam; PF00362; integrin_B; 1.
DR   ProDom; PD001811; Integrin_B; 1.
FT   NON_TER       1      1
FT   NON_TER      50     50
SQ   SEQUENCE   50 AA;  5469 MW;  C82D2269C7016957 CRC64;

  Query Match             100.0%;  Score 20;  DB 5;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 NLDA 4
              ||||
Db         47 NLDA 50
```

Search completed: January 21, 2004, 09:25:10
Job time : 2.826 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 21, 2004, 09:15:44 ; Search time 0.198853 Seconds
(without alignments)
945.960 Million cell updates/sec

Title: US-09-869-414A-66
Perfect score: 20
Sequence: 1 NLDA 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	54	1	VG87_BPMD2	O64268 mycobacteri
2	20	100.0	70	1	RPCX_YEAST	P40422 saccharomyc
3	20	100.0	75	1	TRY3_ECOLI	P05835 escherichia
4	20	100.0	82	1	YNI1_FRAAL	P46041 frankia aln
5	20	100.0	85	1	GLR1_ECOLI	P00277 escherichia
6	20	100.0	89	1	BARS_BACAM	P11540 bacillus am
7	20	100.0	91	1	S112_PIG	P80310 sus scrofa
8	20	100.0	102	1	CMGC_BACHD	Q9k923 bacillus ha
9	20	100.0	103	1	S11Z_HUMAN	Q96fq6 homo sapien
10	20	100.0	109	1	YIR1_YEAST	P40440 saccharomyc
11	20	100.0	114	1	YOAB_ECOLI	P76258 escherichia
12	20	100.0	119	1	ACPS_BACHD	Q9kfg1 bacillus ha
13	20	100.0	119	1	SY24_HUMAN	O00175 homo sapien
14	20	100.0	123	1	AZUP_PARDE	P80649 paracoccus
15	20	100.0	124	1	Y670_PASMU	Q9cmy0 pasteurella
16	20	100.0	125	1	YHEN_PASHA	P95509 pasteurella
17	20	100.0	126	1	CD59_RAT	P27274 rattus norv

18	20	100.0	126	1	PFD4_CAEEL	Q17435 caenorhabdi
19	20	100.0	132	1	FLSA_PSEAE	O33422 pseudomonas
20	20	100.0	133	1	Y044_BORBU	O51073 borrelia bu
21	20	100.0	145	1	AZUP_PARPN	P80401 paracoccus
22	20	100.0	146	1	YN21_DEIRA	Q9rs06 deinococcus
23	20	100.0	150	1	SP0A_BACCE	P52930 bacillus ce
24	20	100.0	157	1	ISPF_LISIN	Q92f39 listeria in
25	20	100.0	157	1	ISPF_LISMO	Q8yab4 listeria mo
26	20	100.0	159	1	GREA_CHLTE	Q8kch5 chlorobium
27	20	100.0	159	1	NIFX_RHOCA	P19078 rhodobacter
28	20	100.0	160	1	FLAV_CLOSA	P18855 clostridium
29	20	100.0	161	1	Y088_BRUME	Q8yjj5 brucella me
30	20	100.0	164	1	PHEA_SYNY1	P20778 synechocyst
31	20	100.0	165	1	LB21_ARATH	Q9srl8 arabidopsis
32	20	100.0	168	1	NUE2_RHIME	P56910 rhizobium m
33	20	100.0	172	1	YFIR_ECOLI	P76597 escherichia
34	20	100.0	176	1	YWY1_CAEEL	Q11088 caenorhabdi
35	20	100.0	184	1	KAD1_ANASP	Q8ypj8 anabaena sp
36	20	100.0	189	1	TBP_THECE	Q56253 thermococcu
37	20	100.0	190	1	TBP_PYRKO	Q52366 pyrococcus
38	20	100.0	191	1	SP0A_BACPU	P52933 bacillus pu
39	20	100.0	191	1	TXLA_SYNP7	P35088 synechococc
40	20	100.0	195	1	IND1_HUMAN	P37290 homo sapien
41	20	100.0	197	1	YDB6_YEAST	Q12055 saccharomyc
42	20	100.0	202	1	GDIR_YEAST	Q12434 saccharomyc
43	20	100.0	203	1	RS4_CHLTE	P59129 chlorobium
44	20	100.0	207	1	COAE_XYLFA	Q9pai2 xylella fas
45	20	100.0	209	1	VS10_ROTBS	P34718 bovine rota

ALIGNMENTS

```
RESULT 1
VG87_BPMD2
ID   VG87_BPMD2     STANDARD;      PRT;    54 AA.
AC   O64268;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Gene 87 protein (GP87).
GN   87.
OS   Mycobacteriophage D29.
OC   Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX   NCBI_TaxID=28369;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98300335; PubMed=9636706;
RA   Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
RT   "Genome structure of mycobacteriophage D29: implications for phage
RT   evolution.";
RL   J. Mol. Biol. 279:143-164(1998).
CC   ------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
```

```
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF022214; AAC18517.1; -.
DR   PIR; C72809; C72809.
SQ   SEQUENCE   54 AA;  6210 MW;  C6D36552F48CE621 CRC64;

  Query Match             100.0%;  Score 20;  DB 1;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db          9 NLDA 12


RESULT 2
RPCX_YEAST
ID   RPCX_YEAST     STANDARD;      PRT;    70 AA.
AC   P40422;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   DNA-directed RNA polymerases I, II, and III 7.7 kDa polypeptide
DE   (EC 2.7.7.6) (ABC10-alpha).
GN   RPC10 OR RPB12 OR YHR143BW.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 4-23 AND 64-70.
RC   STRAIN=S288c;
RX   MEDLINE=92314714; PubMed=1617300;
RA   Treich I., Carles C., Riva M., Sentenac A.;
RT   "RPC10 encodes a new mini subunit shared by yeast nuclear RNA
RT   polymerases.";
RL   Gene Expr. 2:31-37(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c / AB972;
RX   MEDLINE=94378003; PubMed=8091229;
RA   Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA   Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
RA   Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA   Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
RA   Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
RA   Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
RA   Vaudin M.;
RT   "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT   VIII.";
RL   Science 265:2077-2082(1994).
CC   -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC       OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC       SUBSTRATES.
CC   -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
```

```
CC       {RNA}(N).
CC   -!- SUBUNIT: EACH CLASS OF RNA POLYMERASE IS ASSEMBLED FROM 9 TO 15
CC       DIFFERENT POLYPEPTIDES. THIS SUBUNIT IS SHARED BY ALL 3 YEAST RNA
CC       POLYMERASES.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- PTM: THE N-TERMINUS IS BLOCKED.
CC   -!- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE
CC       FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
CC       PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
CC       III FOR 5S AND TRNA GENES.
CC   -!- SIMILARITY: BELONGS TO THE ARCHAEBACTERIA RPOP / EUKARYOTIC RPC10
CC       RNA POLYMERASE SUBUNIT FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U23378; AAA64417.1; -.
DR   EMBL; U10397; AAB68994.1; -.
DR   PIR; S58932; S58932.
DR   PDB; 1I3Q; 18-JUL-01.
DR   PDB; 1I50; 13-JUN-01.
DR   PDB; 1K83; 22-MAY-02.
DR   SGD; S0001185; RPC10.
DR   InterPro; IPR003221; DNA_RNApol_7kD.
DR   InterPro; IPR006591; RNA_pol_Rbp10.
DR   Pfam; PF03604; DNA_RNApol_7kD; 1.
DR   ProDom; PD012151; DNA_RNApol_7kD; 1.
DR   SMART; SM00659; RPOLCX; 1.
KW   Transferase; DNA-directed RNA polymerase; Transcription;
KW   Nuclear protein; Metal-binding; Zinc-finger; 3D-structure.
FT   ZN_FING      31     51       C4-TYPE (POTENTIAL).
SQ   SEQUENCE   70 AA;  7716 MW;  066A3D982EC7361E CRC64;

  Query Match             100.0%;  Score 20;  DB 1;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         11 NLDA 14


RESULT 3
TRY3_ECOLI
ID   TRY3_ECOLI     STANDARD;      PRT;     75 AA.
AC   P05835;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   TraY protein.
GN   TRAY.
OS   Escherichia coli.
```

```
OG   Plasmid IncFII R100-1, and Plasmid IncFII R100.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   PLASMID=IncFII R100-1;
RX   MEDLINE=87008371; PubMed=3531163;
RA   Finlay B.B., Frost L.S., Paranchych W.;
RT   "Origin of transfer of IncF plasmids and nucleotide sequences of the
RT   type II oriT, traM, and traY alleles from ColB4-K98 and the type IV
RT   traY allele from R100-1.";
RL   J. Bacteriol. 168:132-139(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   PLASMID=IncFII R100;
RX   MEDLINE=88227859; PubMed=2836369;
RA   Inamoto S., Yoshioka Y., Ohtsubo E.;
RT   "Identification and characterization of the products from the traJ
RT   and traY genes of plasmid R100.";
RL   J. Bacteriol. 170:2749-2757(1988).
CC   -!- FUNCTION: INVOLVED IN THE CONJUGATION PROCESS OF BACTERIAL CELLS
CC       FOR THE EXCHANGE OF PLASMID DNA. IT IS ALSO RESPONSIBLE FOR
CC       CONJUGAL DNA METABOLISM. TRAY IS REQUIRED FOR STRAND-SPECIFIC
CC       NICKING AT ORIT, THE TRANSFER ORIGIN.
CC   -!- SIMILARITY: TO TRAY PROTEIN OF OTHER PLASMIDS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M15136; AAA26076.1; -.
DR   EMBL; M20941; AAA26073.1; -.
DR   PIR; C25033; BVECRY.
KW   Plasmid; Conjugation; DNA-binding.
SQ   SEQUENCE   75 AA;  8542 MW;  88D4B04C4B5DE07A CRC64;

  Query Match             100.0%;  Score 20;  DB 1;  Length 75;
  Best Local Similarity   100.0%;  Pred. No. 84;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         57 NLDA 60


RESULT 4
YNI1_FRAAL
ID   YNI1_FRAAL     STANDARD;      PRT;    82 AA.
AC   P46041;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
```

```
DE   Hypothetical 9.1 kDa protein in nifX-nifW intergenic region (ORF1).
OS   Frankia alni.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Frankineae; Frankiaceae; Frankia.
OX   NCBI_TaxID=1859;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CpI1;
RX   MEDLINE=95369734; PubMed=7642138;
RA   Harriott O.T., Hosted T.J., Benson D.R.;
RT   "Sequences of nifX, nifW, nifZ, nifB and two ORF in the Frankia
RT   nitrogen fixation gene cluster.";
RL   Gene 161:63-67(1995).
CC   -!- SIMILARITY: TO SIMILAR PROTEINS IN OTHER NITROGEN-FIXING BACTERIA.
CC       THIS PROTEIN IS GENERALLY FOUND IN THE NIFX-NIFW INTERGENIC REGION
CC       OR IN THE FIXX 3'REGION.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L29299; AAC82972.1; -.
DR   PIR; T09234; T09234.
DR   Pfam; PF05082; DUF683; 1.
KW   Hypothetical protein; Nitrogen fixation.
SQ   SEQUENCE   82 AA;  9081 MW;  AFBBD86827B4322C CRC64;

  Query Match             100.0%;  Score 20;  DB 1;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         17 NLDA 20


RESULT 5
GLR1_ECOLI
ID   GLR1_ECOLI     STANDARD;      PRT;    85 AA.
AC   P00277;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Glutaredoxin 1 (Grx1).
GN   GRXA OR GRX OR B0849 OR SF0802.
OS   Escherichia coli, and
OS   Shigella flexneri.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=562, 623;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=E.coli;
```

RX MEDLINE=87005940; PubMed=3530878;
RA Hoeoeg J.-O., von Bahr-Lindstrom H., Joernvall H., Holmgren A.;
RT "Cloning and expression of the glutaredoxin (grx) gene of Escherichia
RT coli.";
RL Gene 43:13-21(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RA Chatterjee P.K., Sternberg N.L.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [5]
RP SEQUENCE.
RC SPECIES=E.coli; STRAIN=K12;
RX MEDLINE=84004402; PubMed=6352262;
RA Hoeoeg J.-O., Joernvall H., Holmgren A., Carlquist M., Persson M.;
RT "The primary structure of Escherichia coli glutaredoxin. Distant
RT homology with thioredoxins in a superfamily of small proteins with a
RT redox-active cystine disulfide/cysteine dithiol.";
RL Eur. J. Biochem. 136:223-232(1983).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [7]
RP STRUCTURE BY NMR.
RC SPECIES=E.coli;

```
RX   MEDLINE=91364685; PubMed=1889405;
RA   Sodano P., Chary K.V.R., Bjoernberg O., Holmgren A., Kren B.,
RA   Fuchs J.A., Wuethrich K.;
RT   "Nuclear magnetic resonance studies of recombinant Escherichia coli
RT   glutaredoxin. Sequence-specific assignments and secondary structure
RT   determination of the oxidized form.";
RL   Eur. J. Biochem. 200:369-377(1991).
RN   [8]
RP   STRUCTURE BY NMR.
RC   SPECIES=E.coli;
RX   MEDLINE=92046066; PubMed=1942053;
RA   Sodano P., Xia T.-H., Bushweller J.H., Bjoernberg O., Holmgren A.,
RA   Billeter M., Wuethrich K.;
RT   "Sequence-specific 1H NMR assignments and determination of the three-
RT   dimensional structure of reduced Escherichia coli glutaredoxin.";
RL   J. Mol. Biol. 221:1311-1324(1991).
RN   [9]
RP   STRUCTURE BY NMR.
RC   SPECIES=E.coli;
RX   MEDLINE=93278264; PubMed=1304339;
RA   Xia T.-H., Bushweller J.H., Sodano P., Billeter M., Bjoernberg O.,
RA   Holmgren A., Wuethrich K.;
RT   "NMR structure of oxidized Escherichia coli glutaredoxin: comparison
RT   with reduced E. coli glutaredoxin and functionally related
RT   proteins.";
RL   Protein Sci. 1:310-321(1992).
RN   [10]
RP   STRUCTURE BY NMR.
RC   SPECIES=E.coli;
RX   MEDLINE=97270442; PubMed=9125525;
RA   Kelley J.J. III, Caputo M., Eaton S.F., Laue T.M., Bushweller J.H.;
RT   "Comparison of backbone dynamics of reduced and oxidized Escherichia
RT   coli glutaredoxin-1 using 15N NMR relaxation measurements.";
RL   Biochemistry 36:5029-5044(1997).
CC   -!- FUNCTION: THE DISULFIDE BOND FUNCTIONS AS AN ELECTRON CARRIER IN
CC       THE GLUTATHIONE-DEPENDENT SYNTHESIS OF DEOXYRIBONUCLEOTIDES BY THE
CC       ENZYME RIBONUCLEOTIDE REDUCTASE. IN ADDITION, IT IS ALSO INVOLVED
CC       IN REDUCING SOME DISULFIDES IN A COUPLED SYSTEM WITH GLUTATHIONE
CC       REDUCTASE.
CC   -!- SUBUNIT: Monomer.
CC   -!- SIMILARITY: BELONGS TO THE GLUTAREDOXIN FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M13449; AAA23936.1; -.
DR   EMBL; U18655; AAC43449.1; -.
DR   EMBL; AE000187; AAC73936.1; -.
DR   EMBL; D90722; BAA35552.1; -.
DR   EMBL; D90723; BAA35560.1; -.
DR   EMBL; AE015109; AAN42435.1; ALT_INIT.
DR   PIR; A00283; GDEC.
```

```
DR   PDB; 1EGO; 31-OCT-93.
DR   PDB; 1EGR; 31-OCT-93.
DR   PDB; 1GRX; 24-JUN-98.
DR   PDB; 1QFN; 01-JAN-00.
DR   ECO2DBASE; B011.0; 6TH EDITION.
DR   EcoGene; EG10417; grxA.
DR   InterPro; IPR002109; Glutaredoxin.
DR   Pfam; PF00462; glutaredoxin; 1.
DR   PRINTS; PR00160; GLUTAREDOXIN.
DR   PROSITE; PS00195; GLUTAREDOXIN; 1.
KW   Redox-active center; Electron transport; 3D-structure;
KW   Deoxyribonucleotide synthesis; Complete proteome.
FT   DISULFID     11     14       REDOX-ACTIVE.
FT   STRAND        2      6
FT   HELIX        12     27
FT   STRAND       32     36
FT   HELIX        38     41
FT   TURN         42     42
FT   HELIX        45     52
FT   TURN         53     53
FT   STRAND       61     64
FT   TURN         65     66
FT   STRAND       67     70
FT   HELIX        72     82
FT   TURN         83     85
SQ   SEQUENCE   85 AA;  9685 MW;  33C185A47021EF42 CRC64;

  Query Match             100.0%;  Score 20;  DB 1;  Length 85;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         82 NLDA 85


RESULT 6
BARS_BACAM
ID   BARS_BACAM     STANDARD;      PRT;    89 AA.
AC   P11540;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Barstar (Ribonuclease inhibitor).
OS   Bacillus amyloliquefaciens.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1390;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89012012; PubMed=3050134;
RA   Hartley R.W.;
RT   "Barnase and barstar. Expression of its cloned inhibitor permits
RT   expression of a cloned ribonuclease.";
RL   J. Mol. Biol. 202:913-915(1988).
RN   [2]
RP   REVIEW.
RX   MEDLINE=90162921; PubMed=2696173;
```

```
RA   Hartley R.W.;
RT   "Barnase and barstar: two small proteins to fold and fit together.";
RL   Trends Biochem. Sci. 14:450-454(1989).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH BARNASE.
RA   Guillet V., Lapthorn A., Hartley R.W., Mauguen Y.;
RT   "Recognition between a bacterial ribonuclease, barnase, and its
RT   natural inhibitor, barstar.";
RL   Structure 1:165-177(1993).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF COMPLEX WITH RNASE SA.
RX   MEDLINE=98437624; PubMed=9757110;
RA   Sevcik J., Urbanikova L., Dauter Z., Wilson K.S.;
RT   "Recognition of RNase Sa by the inhibitor barstar: structure of the
RT   complex at 1.7 A resolution.";
RL   Acta Crystallogr. D 54:954-963(1998).
RN   [5]
RP   STRUCTURE BY NMR.
RX   MEDLINE=94009694; PubMed=8405454;
RA   Lubienski M.J., Bycroft M., Jones D.N.M., Fersht A.R.;
RT   "Assignment of the backbone 1H and 15N NMR resonances and secondary
RT   structure characterization of barstar.";
RL   FEBS Lett. 332:81-87(1993).
RN   [6]
RP   STRUCTURE BY NMR.
RX   MEDLINE=94318630; PubMed=8043574;
RA   Lubienski M.J., Bycroft M., Freund S.M.V., Fersht A.R.;
RT   "Three-dimensional solution structure and 13C assignments of barstar
RT   using nuclear magnetic resonance spectroscopy.";
RL   Biochemistry 33:8866-8877(1994).
CC   -!- FUNCTION: INHIBITOR OF THE RIBONUCLEASE BARNASE. FORMS A ONE-TO-
CC       ONE NON-COVALENT COMPLEX.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X15545; CAA33551.1; -.
DR   PIR; S01373; S01373.
DR   PDB; 1BRS; 31-JUL-94.
DR   PDB; 1BTA; 31-JUL-94.
DR   PDB; 1BTB; 31-JUL-94.
DR   PDB; 1AB7; 04-SEP-97.
DR   PDB; 1A19; 08-APR-98.
DR   PDB; 1B27; 09-DEC-98.
DR   PDB; 1B2S; 09-DEC-98.
DR   PDB; 1B2U; 09-DEC-98.
DR   PDB; 1B3S; 09-DEC-98.
DR   PDB; 1AY7; 02-MAR-99.
DR   PDB; 1BGS; 31-JUL-94.
DR   PDB; 1L1K; 04-DEC-02.
DR   InterPro; IPR000468; Barstar.
```

```
DR   Pfam; PF01337; Barstar; 1.
DR   ProDom; PD029050; Barstar; 1.
KW   3D-structure.
FT   INIT_MET      0      0
FT   STRAND        2      6
FT   HELIX         7      9
FT   HELIX        13     23
FT   TURN         24     25
FT   TURN         28     29
FT   HELIX        34     43
FT   TURN         44     44
FT   STRAND       49     54
FT   TURN         55     55
FT   HELIX        56     62
FT   TURN         63     65
FT   HELIX        66     79
FT   TURN         80     81
FT   STRAND       84     89
SQ   SEQUENCE   89 AA;  10212 MW;  3AC7E76A9C43A505 CRC64;

  Query Match             100.0%;  Score 20;  DB 1;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         33 NLDA 36


RESULT 7
S112_PIG
ID   S112_PIG       STANDARD;      PRT;    91 AA.
AC   P80310;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Calgranulin C (CAGC).
GN   S100A12.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Granulocyte;
RX   MEDLINE=95050708; PubMed=7961855;
RA   Dell'Angelica E.C., Schleicher C.H., Santome J.A.;
RT   "Primary structure and binding properties of calgranulin C, a novel
RT   S100-like calcium-binding protein from pig granulocytes.";
RL   J. Biol. Chem. 269:28929-28936(1994).
CC   -!- TISSUE SPECIFICITY: FOUND ESSENTIALLY IN GRANULOCYTES WITH SMALL
CC       AMOUNTS FOUND IN LYMPHOCYTES.
CC   -!- MISCELLANEOUS: IN THE ABSENCE OF ZINC BINDS ONE CALCIUM ION PER
CC       MOLECULE, IN THE PRESENCE OF ZINC BINDS TWO CALCIUM IONS PER
CC       MOLECULE.
CC   -!- SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC   -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
```

```
DR   PIR; A55406; A55406.
DR   HSSP; P80511; 1E8A.
DR   InterPro; IPR001751; CaBP_S100.
DR   InterPro; IPR002048; EF-hand.
DR   Pfam; PF00036; efhand; 1.
DR   Pfam; PF01023; S_100; 1.
DR   ProDom; PD003407; CaBP_S100; 1.
DR   ProDom; PD000012; EF-hand; 1.
DR   PROSITE; PS00018; EF_HAND; FALSE_NEG.
DR   PROSITE; PS00303; S100_CABP; 1.
KW   Calcium-binding; Zinc; Metal-binding.
FT   CA_BIND      18     31       EF-HAND 1 (LOW AFFINITY) (BY SIMILARITY).
FT   CA_BIND      61     72       EF-HAND 2 (HIGH AFFINITY) (BY
FT                                SIMILARITY).
SQ   SEQUENCE   91 AA;  10614 MW;  B4204461432D7FCE CRC64;

  Query Match             100.0%;  Score 20;  DB 1;  Length 91;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         59 NLDA 62


RESULT 8
CMGC_BACHD
ID   CMGC_BACHD     STANDARD;      PRT;   102 AA.
AC   Q9K923;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   ComG operon protein 3 homolog precursor.
GN   COMGC OR BH2827.
OS   Bacillus halodurans.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=86665;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C-125 / JCM 9153;
RX   MEDLINE=20512582; PubMed=11058132;
RA   Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA   Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA   Horikoshi K.;
RT   "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT   halodurans and genomic sequence comparison with Bacillus subtilis.";
RL   Nucleic Acids Res. 28:4317-4331(2000).
CC   -!- FUNCTION: Required for transformation and DNA-binding (By
CC       similarity).
CC   -!- SUBUNIT: Homodimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: The unprocessed form is an integral membrane
CC       protein with its C-terminus outside the membrane. Upon cleavage,
CC       it is translocated to the outer face of the membrane (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the comGC family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
```

```
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AP001516; BAB06546.1; -.
DR   PIR; C84003; C84003.
DR   InterPro; IPR000983; Bac_GSPG.
DR   InterPro; IPR001120; Prok_N_methyltn.
DR   PRINTS; PR00813; BCTERIALGSPG.
DR   PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
KW   Competence; Transport; Methylation; Transmembrane; Complete proteome.
FT   PROPEP          1     10       BY SIMILARITY.
FT   CHAIN          11    102       COMG OPERON PROTEIN 3 HOMOLOG.
FT   TRANSMEM       11     31       POTENTIAL.
FT   MOD_RES        11     11       METHYLATION (BY SIMILARITY).
FT   DISULFID       46     85       BY SIMILARITY.
SQ   SEQUENCE   102 AA;  11368 MW;  3C4BD89B08564A43 CRC64;

  Query Match             100.0%;  Score 20;  DB 1;  Length 102;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         70 NLDA 73


RESULT 9
S11Z_HUMAN
ID   S11Z_HUMAN     STANDARD;      PRT;   103 AA.
AC   Q96FQ6;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Putative S100 calcium-binding protein MGC17528.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain, and Cervix;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
```

```
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC   -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; BC010541; AAH10541.1; -.
DR   EMBL; BC019099; AAH19099.1; -.
DR   InterPro; IPR001751; CaBP_S100.
DR   InterPro; IPR002048; EF-hand.
DR   Pfam; PF00036; efhand; 1.
DR   ProDom; PD003407; CaBP_S100; 1.
DR   PROSITE; PS00018; EF_HAND; 1.
DR   PROSITE; PS00303; S100_CABP; 1.
KW   Hypothetical protein; Calcium-binding.
FT   CA_BIND      23     36       EF-HAND 1 (LOW AFFINITY) (POTENTIAL).
FT   CA_BIND      67     78       EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).
SQ   SEQUENCE   103 AA;  11801 MW;  7D00C08F85697A6C CRC64;

  Query Match             100.0%;  Score 20;  DB 1;  Length 103;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         65 NLDA 68


RESULT 10
YIR1_YEAST
ID   YIR1_YEAST     STANDARD;      PRT;   109 AA.
AC   P40440;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Hypothetical 11.6 kDa protein in SDL1 5'region.
GN   YIL171W OR YI9402.06A.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RC   STRAIN=S288c / AB972;
RX   PubMed=9169870;
RA   Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
RA   Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
RA   Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
RA   Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
RA   Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;
RT   "The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";
RL   Nature 387:84-87(1997).
CC   -!- FUNCTION: PROBABLE GLUCOSE TRANSPORTER.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC   -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
CC   -!- CAUTION: YIL171W AND YIL170W REPRESENT THE N- AND C-TERMINAL
CC       OF A PUTATIVE TRANSPORTER.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z46881; CAA87021.1; -.
DR   PIR; S50356; S50356.
DR   SGD; S0001433; HXT12.
DR   InterPro; IPR005828; Sub_transporter.
DR   Pfam; PF00083; sugar_tr; 1.
KW   Hypothetical protein; Repeat; Transmembrane; Sugar transport;
KW   Transport; Glycoprotein.
FT   DOMAIN        1     56       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     57     77       POTENTIAL.
FT   DOMAIN       78    109       EXTRACELLULAR (POTENTIAL).
FT   CARBOHYD     87     87       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   109 AA;  11638 MW;  B9316C3626558434 CRC64;

  Query Match             100.0%;  Score 20;  DB 1;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         40 NLDA 43


RESULT 11
YOAB_ECOLI
ID   YOAB_ECOLI     STANDARD;      PRT;   114 AA.
AC   P76258;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Hypothetical protein yoaB.
GN   YOAB OR B1809 OR C2213 OR SF1419.
OS   Escherichia coli,
OS   Escherichia coli O6, and
OS   Shigella flexneri.
```

```
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=562, 217992, 623;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=E.coli; STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=E.coli; STRAIN=K12;
RX   MEDLINE=97251358; PubMed=9097040;
RA   Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA   Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA   Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA   Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
RA   Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA   Yamamoto Y., Horiuchi T.;
RT   "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT   corresponding to the 40.1-50.0 min region on the linkage map.";
RL   DNA Res. 3:379-392(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   SPECIES=E.coli; STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX   MEDLINE=22388234; PubMed=12471157;
RA   Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA   Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA   Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA   Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT   "Extensive mosaic structure revealed by the complete genome sequence
RT   of uropathogenic Escherichia coli.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX   MEDLINE=22272406; PubMed=12384590;
RA   Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA   Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA   Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA   Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA   Yu J.;
RT   "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT   through comparison with genomes of Escherichia coli K12 and O157.";
RL   Nucleic Acids Res. 30:4432-4441(2002).
CC   -!- SIMILARITY: BELONGS TO THE UPF0076 (UK114) FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
```

```
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AE000275; AAC74879.1; ALT_INIT.
DR   EMBL; D90825; BAA15618.1; ALT_INIT.
DR   EMBL; AE016761; AAN80672.1; ALT_INIT.
DR   EMBL; AE015166; AAN43020.1; ALT_INIT.
DR   HSSP; P37552; 1QD9.
DR   EcoGene; EG13514; yoaB.
DR   InterPro; IPR006175; Endoribon_LPSP.
DR   InterPro; IPR006056; YjgF-like.
DR   Pfam; PF01042; ribonuc_L-PSP; 1.
DR   PROSITE; PS01094; UPF0076; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   114 AA;  12493 MW;  CB276C49F32AB754 CRC64;

  Query Match             100.0%;  Score 20;  DB 1;  Length 114;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         30 NLDA 33


RESULT 12
ACPS_BACHD
ID   ACPS_BACHD     STANDARD;      PRT;   119 AA.
AC   Q9KFG1;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE   (4'-phosphopantetheinyl transferase acpS).
GN   ACPS OR BH0518.
OS   Bacillus halodurans.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=86665;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C-125 / JCM 9153;
RX   MEDLINE=20512582; PubMed=11058132;
RA   Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA   Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA   Horikoshi K.;
RT   "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT   halodurans and genomic sequence comparison with Bacillus subtilis.";
RL   Nucleic Acids Res. 28:4317-4331(2000).
CC   -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC       A to a Ser of acyl-carrier protein (By similarity).
CC   -!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC       3',5'-bisphosphate + holo-[acyl-carrier protein].
CC   -!- COFACTOR: Magnesium (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
CC       FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
```

```
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AP001508; BAB04237.1; -.
DR   PIR; F83714; F83714.
DR   HAMAP; MF_00101; -; 1.
DR   InterPro; IPR002582; ACPS.
DR   InterPro; IPR004568; Pantethn_trn.
DR   Pfam; PF01648; ACPS; 1.
DR   ProDom; PD004282; ACPS; 1.
DR   TIGRFAMs; TIGR00516; acpS; 1.
DR   TIGRFAMs; TIGR00556; pantethn_trn; 1.
KW   Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
KW   Complete proteome.
FT   METAL         8      8       MAGNESIUM (BY SIMILARITY).
FT   METAL        58     58       MAGNESIUM (BY SIMILARITY).
SQ   SEQUENCE   119 AA;  13421 MW;  2279E552549041C9 CRC64;

  Query Match             100.0%;  Score 20;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         92 NLDA 95


RESULT 13
SY24_HUMAN
ID   SY24_HUMAN     STANDARD;      PRT;   119 AA.
AC   O00175;
DT   15-JUL-1999 (Rel. 38, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Small inducible cytokine A24 precursor (CCL24) (Myeloid progenitor
DE   inhibitory factor-2) (MPIF-2) (CK-beta-6) (Eotaxin-2).
GN   CCL24 OR SCYA24 OR MPIF2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 27-41 AND 73.
RC   TISSUE=Monocytes;
RX   MEDLINE=97258609; PubMed=9104803;
RA   Patel V.P., Kreider B.L., Li Y., Li H., Leung K., Salcedo T.,
RA   Nardelli B., Pippalla V., Gentz S., Thotakura R., Parmelee D.,
RA   Gentz R., Garotta G.;
RT   "Molecular and functional characterization of two novel human C-C
RT   chemokines as inhibitors of two distinct classes of myeloid
RT   progenitors.";
RL   J. Exp. Med. 185:1163-1172(1997).
RN   [2]
```

```
RP   SEQUENCE FROM N.A., AND SEQUENCE OF N-TERMINUS.
RC   TISSUE=Monocytes;
RX   MEDLINE=98030404; PubMed=9365122;
RA   White J.R., Imburgia C., Dul E., Appelbaum E., O'Donnell K.,
RA   O'Shannessy D.J., Brawner M., Fornwald J., Adamou J.,
RA   Elshourbagy N.A., Kaiser K., Foley J.J., Schmidt D.B., Johanson K.,
RA   Macphee C., Moores K., McNulty D., Scott G.F., Schleimer R.P.,
RA   Sarau H.M.;
RT   "Cloning and functional characterization of a novel human CC chemokine
RT   that binds to the CCR3 receptor and activates human eosinophils.";
RL   J. Leukoc. Biol. 62:667-675(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Jones K., Graves T., Duckels G., Fronick W.;
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 3-117 FROM N.A.
RA   Hein H., Theran L.;
RT   "cDNA,genomic organisation and chromosomal location of the MPIF-2
RT   (eotaxin-2) gene.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   STRUCTURE BY NMR.
RX   MEDLINE=20374512; PubMed=10913244;
RA   Mayer K.L., Stone M.J.;
RT   "NMR solution structure and receptor peptide binding of the CC
RT   chemokine eotaxin-2.";
RL   Biochemistry 39:8382-8395(2000).
CC   -!- FUNCTION: CHEMOTACTIC FOR RESTING T LYMPHOCYTES, AND EOSINOPHILS.
CC       HAS LOWER CHEMOTACTIC ACTIVITY FOR NEUTROPHILS BUT NONE FOR
CC       MONOCYTES AND ACTIVATED LYMPHOCYTES. IS A STRONG SUPPRESSOR OF
CC       COLONY FORMATION BY A MULTIPOTENTIAL HEMATOPOIETIC PROGENITOR CELL
CC       LINE. BINDS TO CCR3.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: ACTIVATED MONOCYTES AND ACTIVATED T
CC       LYMPHOCYTES.
CC   -!- PTM: N-GLYCOSYLATED.
CC   -!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC       C-C) (CHEMOKINE CC).
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U85768; AAB51135.1; -.
DR   EMBL; AC005102; AAD15410.1; -.
DR   EMBL; AJ223461; CAA11383.1; -.
DR   PDB; 1EIG; 06-DEC-00.
DR   PDB; 1EIH; 06-DEC-00.
DR   Genew; HGNC:10623; CCL24.
DR   GO; GO:0008009; F:chemokine activity; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0006935; P:chemotaxis; TAS.
```

```
DR   GO; GO:0006955; P:immune response; TAS.
DR   GO; GO:0006954; P:inflammatory response; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR000827; CC_chemkine_sml.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   Pfam; PF00048; IL8; 1.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00472; SMALL_CYTOKINES_CC; FALSE_NEG.
KW   Cytokine; Chemotaxis; Signal; Glycoprotein; Inflammatory response;
KW   3D-structure.
FT   SIGNAL        1     26
FT   CHAIN        27    119       SMALL INDUCIBLE CYTOKINE A24.
FT   DISULFID     33     58
FT   DISULFID     34     74
FT   CARBOHYD    115    115       N-LINKED (GLCNAC. . .).
FT   CONFLICT     61     61        A -> G (IN REF. 1).
FT   CONFLICT     73     73        F -> S (IN REF. 1; AA SEQUENCE).
FT   STRAND       37     37
FT   TURN         44     46
FT   STRAND       47     53
FT   STRAND       62     67
FT   STRAND       72     75
FT   TURN         77     78
FT   HELIX        80     90
FT   HELIX        91     93
FT   TURN         94     94
SQ   SEQUENCE   119 AA;  13133 MW;  6CAACA61731FB393 CRC64;

  Query Match             100.0%;  Score 20;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         88 NLDA 91


RESULT 14
AZUP_PARDE
ID   AZUP_PARDE     STANDARD;      PRT;   123 AA.
AC   P80649;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Pseudoazurin.
OS   Paracoccus denitrificans.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC   Rhodobacteraceae; Paracoccus.
OX   NCBI_TaxID=266;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=NCIMB 8944;
RX   MEDLINE=97184655; PubMed=9032456;
RA   Leung Y.-C., Chan C., Reader J.S., Willis A.C., van Spanning R.J.M.,
RA   Ferguson S.J., Radford S.E.;
RT   "The pseudoazurin gene from Thiosphaera pantotropha: analysis of
RT   upstream putative regulatory sequences and overexpression in
```

```
RT   Escherichia coli.";
RL   Biochem. J. 321:699-705(1997).
CC   -!- FUNCTION: THIS SOLUBLE ELECTRON TRANSFER COPPER PROTEIN IS
CC       REQUIRED FOR THE INACTIVATION OF COPPER-CONTAINING NITRITE
CC       REDUCTASE IN THE PRESENCE OF OXYGEN.
CC   -!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
CC   -!- SIMILARITY: Contains 1 plastocyanin-like domain.
DR   HSSP; P80401; 1ADW.
DR   InterPro; IPR000923; BlueCu_1.
DR   InterPro; IPR001235; Copper_blue.
DR   Pfam; PF00127; copper-bind; 1.
DR   PRINTS; PR00156; COPPERBLUE.
DR   ProDom; PD001235; Copper_blue; 1.
DR   PROSITE; PS00196; COPPER_BLUE; 1.
KW   Copper; Electron transport; Periplasmic.
FT   DOMAIN        5     93       PLASTOCYANIN-LIKE.
FT   METAL        40     40       COPPER (BY SIMILARITY).
FT   METAL        78     78       COPPER (BY SIMILARITY).
FT   METAL        81     81       COPPER (BY SIMILARITY).
FT   METAL        86     86       COPPER (BY SIMILARITY).
SQ   SEQUENCE   123 AA;  13337 MW;  983800FB8B5589E2 CRC64;

  Query Match             100.0%;  Score 20;  DB 1;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NLDA 4
              ||||
Db         98 NLDA 101


RESULT 15
Y670_PASMU
ID   Y670_PASMU     STANDARD;      PRT;   124 AA.
AC   Q9CMY0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Hypothetical protein PM0670 precursor.
GN   PM0670.
OS   Pasteurella multocida.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC   Pasteurellaceae; Pasteurella.
OX   NCBI_TaxID=747;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Pm70;
RX   MEDLINE=21145866; PubMed=11248100;
RA   May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT   "Complete genomic sequence of Pasteurella multocida Pm70.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME B562 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; AE006103; AAK02754.1; -.
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 124 HYPOTHETICAL PROTEIN PM0670.
SQ SEQUENCE 124 AA; 13746 MW; D7B2B485C7B51B9A CRC64;

Query Match 100.0%; Score 20; DB 1; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 NLDA 4
              ||||
Db        101 NLDA 104
```

Search completed: January 21, 2004, 09:23:07
Job time : 2.19885 secs